



HS

1

SEQUENCE LISTING

<110> Bejanin, Stephan
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 142.US5.REG

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<141> 2001-10-15

<150> 60/311,305

<151> 2001-08-10

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gaa ttt gca cgt ata tgc cga gat ctc agc cat att gga gat gct gtt 284
Glu Phe Ala Arg Ile Cys Arg Asp Leu Ser His Ile Gly Asp Ala Val
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Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu
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ctt gga aat gga aac att aaa ttg tca cag aca agt aat gtc gat aaa 380
Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser Asn Val Asp Lys
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55                               60                               65
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Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser
70                               75                               80
tca acg gtg aca ctc agt atg tct gca gat gta ccc ctt gtt gta gag 524
Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu
85                               90                               95                               100
tat aaa att gcg gat atg gga cac tta aaa tac tac ttg gct ccc aag 572
Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys
105                               110                               115
atc gag gat gaa gaa gga tct taggcattct taaaattcaa gaaaataaaaa 623
Ile Glu Asp Glu Glu Gly Ser
120
ctaagctctt tgagaactgc ttctaagatg ccagcatata ctgaagtctt ttctgtcacc 683
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Ala Ser Gly Glu Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser
35                               40                               45
Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro
50                               55                               60
Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala
65                               70                               75                               80
Thr Pro Leu Ser Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro
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Leu Val Val Glu Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr
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Leu Ala Pro Lys Ile Glu Asp Glu Glu Gly Ser
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 Met Gln Asp Glu Asp Gly Tyr Ile
 1 5
 acc tta aat att aaa act cgg aaa cca gct ctc gtc tcc gtt ggc tct 162
 Thr Leu Asn Ile Lys Thr Arg Lys Pro Ala Leu Val Ser Val Gly Ser
 10 15 20
 gca tcc tcc tcc tgg tgg cgt gtg atg gct ttg att ctg ctg atc ctg 210
 Ala Ser Ser Ser Trp Trp Arg Val Met Ala Leu Ile Leu Leu Ile Leu
 25 30 35 40
 tgc gtg ggg atg gtt gtc ggg ctg gtg gct ctg ggg att tgg tct gtc 258
 Cys Val Gly Met Val Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val
 45 50 55
 atg cag cgc aat tac cta caa gat gag aat gaa aat cgc aca gga act 306
 Met Gln Arg Asn Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr
 60 65 70
 ctg caa caa tta gca aag cgc ttc tgt caa tat gtg gta aaa caa tca 354
 Leu Gln Gln Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser
 75 80 85
 gaa cta aag ggc act ttc aaa ggt cat aaa tgc agc ccc tgt gac aca 402
 Glu Leu Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr
 90 95 100
 aac tgg aga tat tat gga gat agc tgc tat ggg ttc ttc agg cac aac 450
 Asn Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn
 105 110 115 120
 tta aca tgg gaa gag agt aag cag tac tgc act gac atg aat gct act 498
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 125 130 135
 ctc ctg aag att gac aac cgg aac att gtg gag tac atc aaa gcc agg 546

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Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys Ala Arg
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act cat tta att cgt tgg gtc gga tta tct cgc cag aag tcg aat gag 594
Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys Ser Asn Glu
      155      160      165
gtc tgg aag tgg gag gat ggc tcg gtt atc tca gaa aat atg ttt gag 642
Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu Asn Met Phe Glu
      170      175      180
ttt ttg gaa gat gga aaa gga aat atg aat tgt gct tat ttt cat aat 690
Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys Ala Tyr Phe His Asn
      185      190      195      200
ggg aaa atg cac cct acc ttc tgt gag aac aaa cat tat tta atg tgt 738
Gly Lys Met His Pro Thr Phe Cys Glu Asn Lys His Tyr Leu Met Cys
      205      210      215
gag agg aag gct ggc atg acc aag gtg gac caa cta cct taatgcaaag 787
Glu Arg Lys Ala Gly Met Thr Lys Val Asp Gln Leu Pro
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Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val Val Gly Leu
      35      40      45
Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp
      50      55      60
Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe
      65      70      75      80
Cys Gln Tyr Val Val Lys Gln Ser Glu Leu Lys Gly Thr Phe Lys Gly
      85      90      95
His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser
      100      105      110
Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln
      115      120      125
Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg Asn
      130      135      140
Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val Gly
      145      150      155      160
Leu Ser Arg Gln Lys Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser
      165      170      175
Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn
      180      185      190
Met Asn Cys Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys
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 aacacaccaa ggaaaattaa tataggaaaa atttaaaaaag ttattagagg actgaaaata 180
 taaaaaatgga acactgaaaag acacagagtt tttattttca gcaactgcagc tctg atg 237
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 gtc cag ctc cac cag gac aca gat ccc cag atc cct aaa ggt cag cca 285
 Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln Pro
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 tgc acc ctg aac agc tca gag gga gga gcc agg cca gca gtg cct cac 333
 Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro His
 20 25 30
 acc ttg ttc tct tct gct cta gac aga tgg ctc cat aat gac agc ttc 381
 Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser Phe
 35 40 45
 ata atg gca gtg ggt gag ccc ctg gtg cac atc agg gtc act ctt ctg 429
 Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu Leu
 50 55 60 65
 ctg ctc tgg ttt gga atg ttt ttg tct att tct ggc cac tct cag gcc 477
 Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln Ala
 70 75 80
 agg ccc tcc cag tat ttc act tct cca gaa gtg gtg atc cct ttg aag 525
 Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu Lys
 85 90 95
 gtg atc agc agg ggc aga ggt gca aag gct cct gga tgg ctc tcc tat 573
 Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser Tyr
 100 105 110
 agc ctg cgg ttt ggg gga cag aga tac att gtc cac atg agg gta aat 621
 Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val Asn
 115 120 125
 aag ctg ttg ttt gct gca cac ctt cct gtg ttc acc tac aca gag cag 669
 Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu Gln
 130 135 140 145
 cat gcc ctg ctc cag gat cag ccc ttc atc cag gat gac tgc tac tac 717
 His Ala Leu Leu Gln Asp Gln Pro Phe Ile Gln Asp Asp Cys Tyr Tyr
 150 155 160
 cat ggt tat gtg gag ggg gtc cct gag tcc ttg gtt gcc ctt agt acc 765

His Gly Tyr Val Glu Gly Val Pro Glu Ser Leu Val Ala Leu Ser Thr	
165 170 175	
tgt tct ggg ggc ttt ctt gga atg cta cag ata aat gac ctt gtt tat	813
Cys Ser Gly Gly Phe Leu Gly Met Leu Gln Ile Asn Asp Leu Val Tyr	
180 185 190	
gaa atc aag cca att agt gtt tct gcc aca ttt gaa cac cta gta tat	861
Glu Ile Lys Pro Ile Ser Val Ser Ala Thr Phe Glu His Leu Val Tyr	
195 200 205	
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Lys Ile Asp Ser Asp Asp Thr Gln Phe Pro Pro Met Arg Cys Gly Leu	
210 215 220 225	
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Thr Glu Glu Lys Ile Ala His Gln Met Glu Leu Gln Leu Ser Tyr Asn	
230 235 240	
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245 250 255	
ttt gtt gag ctg gta gtg gtc gtg gat aat att aga tat ctt ttc tct	1053
Phe Val Glu Leu Val Val Val Val Asp Asn Ile Arg Tyr Leu Phe Ser	
260 265 270	
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275 280 285	
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Gly Ile Asp Ile Trp Thr Ala Ser Asn Pro Leu Pro Thr Ser Gly Asp	
310 315 320	
cta gat aat gtt tta gag gac ttt tct att tgg aag aat tat aac ctt	1245
Leu Asp Asn Val Leu Glu Asp Phe Ser Ile Trp Lys Asn Tyr Asn Leu	
325 330 335	
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Asn Asn Arg Leu Gln His Asp Val Ala His Leu Phe Ile Lys Asp Thr	
340 345 350	
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Gln Gly Met Lys Leu Gly Val Ala Tyr Val Lys Gly Ile Cys Gln Asn	
355 360 365	
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Pro Phe Asn Thr Gly Val Asp Val Phe Glu Asp Asn Arg Leu Val Val	
370 375 380 385	
ttt gca att act ttg ggc cac gag ctt ggt cat aat ttg ggt atg caa	1437
Phe Ala Ile Thr Leu Gly His Glu Leu Gly His Asn Leu Gly Met Gln	
390 395 400	
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His Asp Thr Gln Trp Cys Val Cys Glu Leu Gln Trp Cys Ile Met His	
405 410 415	
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Ala Tyr Arg Lys Val Thr Thr Lys Phe Ser Asn Cys Ser Tyr Ala Gln	
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Tyr Trp Asp Ser Thr Ile Ser Ser Gly Leu Cys Ile Gln Pro Pro Pro	
435 440 445	
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Asp Pro Cys Cys Leu Leu Asn Cys Thr Leu His Pro Gly Ala Ala Cys	
485 490 495	
gct ttt gga ata tgt tgc aaa gac tgc aaa ttt ctg cca tca gga act	1773
Ala Phe Gly Ile Cys Cys Lys Asp Cys Lys Phe Leu Pro Ser Gly Thr	
500 505 510	
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515 520 525	
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Gly Thr Ser His Gln Cys Pro Asp Asp Val Tyr Val Gln Asp Gly Ile	
530 535 540 545	
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Ser Cys Asn Val Asn Ala Phe Cys Tyr Glu Lys Thr Cys Asn Asn His	
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565 570 575	
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Gln Ser Cys Tyr Gln Glu Ile Asn Thr Gln Gly Asn Arg Phe Gly His	
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Cys Gly Ile Val Gly Thr Thr Tyr Val Lys Cys Trp Thr Pro Asp Ile	
595 600 605	
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645 650 655	
gtg aaa gat ggc aca gta tgt ggt cca gaa aag atc tgc atc cgt aag	2253
Val Lys Asp Gly Thr Val Cys Gly Pro Glu Lys Ile Cys Ile Arg Lys	
660 665 670	
aag tgt gcc agt atg gtt cat ctg tca caa gcc tgt cag cct aag acc	2301
Lys Cys Ala Ser Met Val His Leu Ser Gln Ala Cys Gln Pro Lys Thr	
675 680 685	
tgc aac atg agg gga atc tgc aac aac aaa caa cac tgt cac tgc aac	2349
Cys Asn Met Arg Gly Ile Cys Asn Asn Lys Gln His Cys His Cys Asn	
690 695 700 705	
cat gaa tgg gca ccc cca tac tgc aag gac aaa ggc tat gga ggt agt	2397
His Glu Trp Ala Pro Pro Tyr Cys Lys Asp Lys Gly Tyr Gly Gly Ser	
710 715 720	
gct gat agt ggc cca cct cct aag aac aac atg gaa gga tta aat gtg	2445
Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn Val	
725 730 735	
atg gga aag ttg cgt tac ctg tca cta ttg tgc ctt ctt cct ttg gtt	2493
Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu Val	
740 745 750	
gct ttt tta tta ttt tgc tta cat gtg ctt ttt aag aaa cgc aca aaa	2541
Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr Lys	

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755              760              765
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<211> 776

<212> PRT

<213> Homo sapiens

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His Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser
35              40              45
Phe Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu
50              55              60
Leu Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln
65              70              75              80
Ala Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu
85              90              95
Lys Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser
100             105             110
Tyr Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val
115             120             125
Asn Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu
130             135             140
Gln His Ala Leu Leu Gln Asp Gln Pro Phe Ile Gln Asp Asp Cys Tyr
145             150             155             160
Tyr His Gly Tyr Val Glu Gly Val Pro Glu Ser Leu Val Ala Leu Ser
165             170             175
Thr Cys Ser Gly Gly Phe Leu Gly Met Leu Gln Ile Asn Asp Leu Val
180             185             190
Tyr Glu Ile Lys Pro Ile Ser Val Ser Ala Thr Phe Glu His Leu Val
195             200             205
Tyr Lys Ile Asp Ser Asp Asp Thr Gln Phe Pro Pro Met Arg Cys Gly
210             215             220
Leu Thr Glu Glu Lys Ile Ala His Gln Met Glu Leu Gln Leu Ser Tyr
225             230             235             240
Asn Phe Thr Leu Lys Gln Ser Ser Phe Val Gly Trp Trp Thr His Gln
245             250             255
Arg Phe Val Glu Leu Val Val Val Val Asp Asn Ile Arg Tyr Leu Phe
260             265             270

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      290                      295                      300
Thr Gly Ile Asp Ile Trp Thr Ala Ser Asn Pro Leu Pro Thr Ser Gly
305                      310                      315                      320
Asp Leu Asp Asn Val Leu Glu Asp Phe Ser Ile Trp Lys Asn Tyr Asn
      325                      330                      335
Leu Asn Asn Arg Leu Gln His Asp Val Ala His Leu Phe Ile Lys Asp
      340                      345                      350
Thr Gln Gly Met Lys Leu Gly Val Ala Tyr Val Lys Gly Ile Cys Gln
      355                      360                      365
Asn Pro Phe Asn Thr Gly Val Asp Val Phe Glu Asp Asn Arg Leu Val
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Val Phe Ala Ile Thr Leu Gly His Glu Leu Gly His Asn Leu Gly Met
385                      390                      395                      400
Gln His Asp Thr Gln Trp Cys Val Cys Glu Leu Gln Trp Cys Ile Met
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Gln Tyr Trp Asp Ser Thr Ile Ser Ser Gly Leu Cys Ile Gln Pro Pro
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Pro Tyr Pro Gly Asn Ile Phe Arg Leu Lys Tyr Cys Gly Asn Leu Val
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Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Thr Ile Arg Gln Cys Ala
465                      470                      475                      480
Lys Asp Pro Cys Cys Leu Leu Asn Cys Thr Leu His Pro Gly Ala Ala
      485                      490                      495
Cys Ala Phe Gly Ile Cys Cys Lys Asp Cys Lys Phe Leu Pro Ser Gly
      500                      505                      510
Thr Leu Cys Arg Gln Gln Val Gly Glu Cys Asp Leu Pro Glu Trp Cys
      515                      520                      525
Asn Gly Thr Ser His Gln Cys Pro Asp Asp Val Tyr Val Gln Asp Gly
      530                      535                      540
Ile Ser Cys Asn Val Asn Ala Phe Cys Tyr Glu Lys Thr Cys Asn Asn
545                      550                      555                      560
His Asp Ile Gln Cys Lys Glu Ile Phe Gly Gln Asp Ala Arg Ser Ala
      565                      570                      575
Ser Gln Ser Cys Tyr Gln Glu Ile Asn Thr Gln Gly Asn Arg Phe Gly
      580                      585                      590
His Cys Gly Ile Val Gly Thr Thr Tyr Val Lys Cys Trp Thr Pro Asp
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Ile Met Cys Gly Arg Val Gln Cys Glu Asn Val Gly Val Ile Pro Asn
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625                      630                      635                      640
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Glu Val Lys Asp Gly Thr Val Cys Gly Pro Glu Lys Ile Cys Ile Arg
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Lys Lys Cys Ala Ser Met Val His Leu Ser Gln Ala Cys Gln Pro Lys
      675                      680                      685
Thr Cys Asn Met Arg Gly Ile Cys Asn Asn Lys Gln His Cys His Cys
      690                      695                      700
Asn His Glu Trp Ala Pro Pro Tyr Cys Lys Asp Lys Gly Tyr Gly Gly
705                      710                      715                      720

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Ser Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn
              725              730              735
Val Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu
              740              745              750
Val Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr
              755              760              765
Lys Ser Lys Glu Asp Glu Glu Gly
              770              775

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<210> 7
<211> 1436
<212> DNA
<213> Homo sapiens

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<220>
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<222> 1..263

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<220>
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<222> 264..926

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<220>
<221> 3'UTR
<222> 927..1436

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<220>
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<222> 1404..1409

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<220>
<221> polyA_site
<222> 1421..1436

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<400> 7
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ccagccaggc tacagggatc gattggagct gtccttgggg ctgtaattgg cccagctga 120
gcagggcaaa cactgaggtc aactacaagc cacaggcccc ttccccagcc tcagttcaca 180
gctgccctgt tgcagggagg cggtggccct tctgttgcta gaccgagcct gtgggatata 240
ccaaggcaga ggagcccata gcc atg agg agc ctc ggg gcc ctg ctc ttg ctg 293
                               Met Arg Ser Leu Gly Ala Leu Leu Leu Leu
                               -15                               -10
ctg agc gcc tgc ctg gcg gtg agc gct ggc cct gtg cca acg ccg ccc 341
Leu Ser Ala Cys Leu Ala Val Ser Ala Gly Pro Val Pro Thr Pro Pro
              -5              1              5
gac aac atc caa gtg cag gaa aac ttc aat atc tct cgg atc tat ggg 389
Asp Asn Ile Gln Val Gln Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly
              10              15              20
aag tgg tac aac ctg gcc atc ggt tcc acc tgc ccc tgg ctg aag aag 437
Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys
              25              30              35
atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga gag ggc gct 485
Ile Met Asp Arg Met Thr Val Ser Thr Leu Val Leu Gly Glu Gly Ala
              40              45              50              55
aca gag gcg gag atc agc atg acc agc act cgt tgg cgg aaa ggt gtc 533
Thr Glu Ala Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Lys Gly Val

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	60	65	70	
tgt gag gag acg tct gga gct tat gag aaa aca gat act gat ggg aag				581
Cys Glu Glu Thr Ser Gly Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys				
	75	80	85	
ttt ctc tat cac aaa tcc aaa tgg aac ata acc atg gag tcc tat gtg				629
Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Met Glu Ser Tyr Val				
	90	95	100	
gtc cac acc aac tat gat gag tat gcc att ttc ctg acc aag aaa ttc				677
Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe				
	105	110	115	
agc cgc cat cat gga ccc acc att act gcc aag ctc tac ggg cgg gcg				725
Ser Arg His His Gly Pro Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala				
	120	125	130	135
ccg cag ctg agg gaa act ctc ctg cag gac ttc aga gtg gtt gcc cag				773
Pro Gln Leu Arg Glu Thr Leu Leu Gln Asp Phe Arg Val Val Ala Gln				
	140	145	150	
ggg gtg ggc atc cct gag gac tcc atc ttc acc atg gct gac cga ggt				821
Gly Val Gly Ile Pro Glu Asp Ser Ile Phe Thr Met Ala Asp Arg Gly				
	155	160	165	
gaa tgt gtc cct ggg gag cag gaa cca gag ccc atc tta atc ccg aga				869
Glu Cys Val Pro Gly Glu Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg				
	170	175	180	
gtc cgg agg gct gct acc cca aga aga gga agg atc agg ggg tgg gca				917
Val Arg Arg Ala Ala Thr Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala				
	185	190	195	
act ggt aac tgaagtcacc aagaaagaag attcctgccca gctgggctac				966
Thr Gly Asn				
200				
tcggccggtc cctgcatggg aatgaccagc aggtatttct ataatgggtac atccatggcc				1026
tgtgagactt tccagtacgg cggctgcatg ggcaacggta acaacttcgt cacagaaaag				1086
gagtgctctgc agacctgccg aactgtggcg gcctgcaatc tccccatagt ccggggccccc				1146
tgccgagcct tcatccagct ctgggcattt gatgctgtca aggggaagtg cgctctcttc				1206
ccctacgggg gctgccaggg caacgggaac aagttctact cagagaagga gtgcagagag				1266
tactgcggtg tccctgggtga tggatgatgag gagctgctgc gcttctccaa ctgacaactg				1326
gccggtctgc aagtcagagg atggccagtg tctgtcccgg ggtcctgtgg caggcagcgc				1386
caagcaacct ggggtccaaat aaaaactaaa ttgcaaaaaa aaaaaaaaaa				1436

<210> 8

<211> 221

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 8

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Val Ser Ala Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln	
	1 5 10
Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala	
	15 20 25
Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr	
	30 35 40 45
Val Ser Thr Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser	

				50					55					60			
Met	Thr	Ser	Thr	Arg	Trp	Arg	Lys	Gly	Val	Cys	Glu	Glu	Thr	Ser	Gly		
			65					70					75				
Ala	Tyr	Glu	Lys	Thr	Asp	Thr	Asp	Gly	Lys	Phe	Leu	Tyr	His	Lys	Ser		
		80					85					90					
Lys	Trp	Asn	Ile	Thr	Met	Glu	Ser	Tyr	Val	Val	His	Thr	Asn	Tyr	Asp		
	95					100					105						
Glu	Tyr	Ala	Ile	Phe	Leu	Thr	Lys	Lys	Phe	Ser	Arg	His	His	Gly	Pro		
110					115					120					125		
Thr	Ile	Thr	Ala	Lys	Leu	Tyr	Gly	Arg	Ala	Pro	Gln	Leu	Arg	Glu	Thr		
				130					135					140			
Leu	Leu	Gln	Asp	Phe	Arg	Val	Val	Ala	Gln	Gly	Val	Gly	Ile	Pro	Glu		
			145					150					155				
Asp	Ser	Ile	Phe	Thr	Met	Ala	Asp	Arg	Gly	Glu	Cys	Val	Pro	Gly	Glu		
		160					165					170					
Gln	Glu	Pro	Glu	Pro	Ile	Leu	Ile	Pro	Arg	Val	Arg	Arg	Ala	Ala	Thr		
	175					180					185						
Pro	Arg	Arg	Gly	Arg	Ile	Arg	Gly	Trp	Ala	Thr	Gly	Asn					
190					195					200							

<210> 9
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<220>
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 <221> 3'UTR
 <222> 552..2132

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<220>
 <221> polyA_site
 <222> 2117..2132

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ctggtggctg	gtctgcaggg	ttgacctgcg	ca atg cag agg	ctg cag gta	gtg											113	
			Met Gln Arg	Leu Gln Val	Val												
			-35		-30												
ctg ggc cac	ctg agg ggt	ccg gcc gat	tcc ggc tgg	atg ccg cag	gcc											161	
Leu Gly His	Leu Arg Gly	Pro Ala Asp	Ser Gly Trp	Met Pro Gln	Ala												
	-25		-20		-15												
gcg cct tgc	ctg agc ggt	gcc ccg cag	gcc tcg gcc	gcg gac gtg	gtg											209	
Ala Pro Cys	Leu Ser Gly	Ala Pro Gln	Ala Ser Ala	Ala Asp Val	Val												
	-10		-5		1												

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gtg gtg cac ggg cgg cgc acg gcc atc tgc cgg gcg ggc cgc ggc ggc 257
Val Val His Gly Arg Arg Thr Ala Ile Cys Arg Ala Gly Arg Gly Gly
5 10 15 20
ttc aag gac acc acc ccc gac gag ctt ctc tgc gca gtc atg acc gcg 305
Phe Lys Asp Thr Thr Pro Asp Glu Leu Leu Ser Ala Val Met Thr Ala
25 30 35
gtt ctc aag gac gtg aat ctg agg ccg gaa cag ctg ggg gac atc tgt 353
Val Leu Lys Asp Val Asn Leu Arg Pro Glu Gln Leu Gly Asp Ile Cys
40 45 50
gtc gga aat gtg ctg cag cct ggg gcc ggg gca atc atg gcc cga atc 401
Val Gly Asn Val Leu Gln Pro Gly Ala Gly Ala Ile Met Ala Arg Ile
55 60 65
gcc cag ttt ctg agt gac atc ccg gag act gtg cct ttg tcc act gtc 449
Ala Gln Phe Leu Ser Asp Ile Pro Glu Thr Val Pro Leu Ser Thr Val
70 75 80
aat aga cag tgt tgc tgc ggg cta cag gca gtg gcc agc ata gca ggg 497
Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Ser Ile Ala Gly
85 90 95 100
tgg agt cca tgt ccc tgg ctg aca gag gga acc ctg gaa ata tta ctt 545
Trp Ser Pro Cys Pro Trp Leu Thr Glu Gly Thr Leu Glu Ile Leu Leu
105 110 115
cgc gct tgatggagaa ggagaaggcc agagattgcc tgattcctat ggggataacc 601
Arg Ala
tctgagaatg tggtgagcg gtttggcatt tcacgggaga agcaggatac ctttgccttg 661
gcttcccagc agaaggcagc aagagcccag agcaagggct gtttccaagc tgagattgtg 721
cctgtgacca ccacgggtcca tgatgacaag ggcaccaaga ggagcatcac tgtgaccag 781
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cgctgccgtc ttggaatacc ctgggaactg agtgagggtcc caggctggag gcgctacgca 1801
gacagtccctg ctgctctagc agcaaggcag taacaccaca aaagcaaaac cacatgggaa 1861
aactcagcac tgggtgggtgt ggcagtggac agatcaaggc acttcaactc atttggaaaa 1921
tgtgaacact gatgacatgg tataggagtg ggtgggggtg tgagccaccc atcagaccct 1981
ctttagctgt gcaagataaa agcagcctgg gtcacccagg ccacaaggcc atggttaatt 2041
cttaaggcaa ggcaaatacca tggatgagaa gtgcaatggg catagtaaaa gtgcatgaat 2101
ttatcttaaa aaaagaaaaa aaaaaaaaaa a 2132

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<210> 10

<211> 153

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..35

<400> 10

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-35          -30          -25          -20
Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
          -15          -10          -5
Ala Ser Ala Ala Asp Val Val Val Val His Gly Arg Arg Thr Ala Ile
          1          5          10
Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
          15          20          25
Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
30          35          40          45
Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
          50          55          60
Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu
          65          70          75
Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln
          80          85          90
Ala Val Ala Ser Ile Ala Gly Trp Ser Pro Cys Pro Trp Leu Thr Glu
          95          100          105
Gly Thr Leu Glu Ile Leu Leu Arg Ala
110          115

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<210> 11

<211> 2266

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..200

<220>

<221> CDS

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<222> 2233..2238

<220>

<221> polyA_site

<222> 2251..2266

<400> 11

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aacagagcta gactccgtct caagaagaag aagaaggaga agaaggagaa ggagaaggga      60
aaaaagaatc ctcatcatta atgcaagtgg aaggaaactc ttcaccaaag aattgatcac      120
atcatgaaag gtgaaatcat tacggaattg cttaaataata taatttgaat ctggatttaa      180
aaataataaa tgtgatcagg atg ccc ttc tct cat ctg tct acc tac agc ctg      233
          Met Pro Phe Ser His Leu Ser Thr Tyr Ser Leu

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										-20											-15		
gtt	tgg	gtc	atg	gca	gca	gtg	gtg	ctg	tgc	aca	gca	caa	gtg	caa	gtg	281							
Val	Trp	Val	Met	Ala	Ala	Val	Val	Leu	Cys	Thr	Ala	Gln	Val	Gln	Val								
										-10											-5	1	
gtg	acc	cag	gat	gaa	aga	gag	cag	ctg	tac	aca	act	gct	tcc	tta	aaa	329							
Val	Thr	Gln	Asp	Glu	Arg	Glu	Gln	Leu	Tyr	Thr	Thr	Ala	Ser	Leu	Lys								
5											10											15	20
tgc	tct	ctg	caa	aat	gcc	cag	gaa	gcc	ctc	att	gtg	aca	tgg	cag	aaa	377							
Cys	Ser	Leu	Gln	Asn	Ala	Gln	Glu	Ala	Leu	Ile	Val	Thr	Trp	Gln	Lys								
										25											30	35	
aag	aaa	gct	gta	agc	cca	gaa	aac	atg	gtc	acc	ttc	agc	gag	aac	cat	425							
Lys	Lys	Ala	Val	Ser	Pro	Glu	Asn	Met	Val	Thr	Phe	Ser	Glu	Asn	His								
										40											45	50	
ggg	gtg	gtg	atc	cag	cct	gcc	tat	aag	gac	aag	ata	aac	att	acc	cag	473							
Gly	Val	Val	Ile	Gln	Pro	Ala	Tyr	Lys	Asp	Lys	Ile	Asn	Ile	Thr	Gln								
										55											60	65	
ctg	gga	ctc	caa	aac	tca	acc	atc	acc	ttc	tgg	aat	atc	acc	ctg	gag	521							
Leu	Gly	Leu	Gln	Asn	Ser	Thr	Ile	Thr	Phe	Trp	Asn	Ile	Thr	Leu	Glu								
										70											75	80	
gat	gaa	ggg	tgt	tac	atg	tgt	ctc	ttc	aat	acc	ttt	ggt	ttt	ggg	aag	569							
Asp	Glu	Gly	Cys	Tyr	Met	Cys	Leu	Phe	Asn	Thr	Phe	Gly	Phe	Gly	Lys								
85											90											95	100
atc	tca	gga	acg	gcc	tgc	ctc	acc	gtc	tat	gta	cag	ccc	ata	gta	tcc	617							
Ile	Ser	Gly	Thr	Ala	Cys	Leu	Thr	Val	Tyr	Val	Gln	Pro	Ile	Val	Ser								
										105											110	115	
ctt	cac	tac	aaa	ttc	tct	gaa	gac	cac	cta	aat	atc	act	tgc	tct	gcc	665							
Leu	His	Tyr	Lys	Phe	Ser	Glu	Asp	His	Leu	Asn	Ile	Thr	Cys	Ser	Ala								
										120											125	130	
act	gcc	cgc	cca	gcc	ccc	atg	gtc	ttc	tgg	aag	gtc	cct	cgg	tca	ggg	713							
Thr	Ala	Arg	Pro	Ala	Pro	Met	Val	Phe	Trp	Lys	Val	Pro	Arg	Ser	Gly								
										135											140	145	
att	gaa	aat	agt	aca	gtg	act	ctg	tct	cac	cca	aat	ggg	acc	acg	tct	761							
Ile	Glu	Asn	Ser	Thr	Val	Thr	Leu	Ser	His	Pro	Asn	Gly	Thr	Thr	Ser								
										150											155	160	
gtt	acc	agc	atc	ctc	cat	atc	aaa	gac	cct	aag	aat	cag	gtg	ggg	aag	809							
Val	Thr	Ser	Ile	Leu	His	Ile	Lys	Asp	Pro	Lys	Asn	Gln	Val	Gly	Lys								
										165											170	175	
gag	gtg	atc	tgc	cag	gtg	ctg	cac	ctg	ggg	act	gtg	acc	gac	ttt	aag	857							
Glu	Val	Ile	Cys	Gln	Val	Leu	His	Leu	Gly	Thr	Val	Thr	Asp	Phe	Lys								
										185											190	195	
caa	acc	gtc	aac	aaa	ggc	tat	tgg	ttt	tca	gtt	ccg	cta	ttg	cta	agc	905							
Gln	Thr	Val	Asn	Lys	Gly	Tyr	Trp	Phe	Ser	Val	Pro	Leu	Leu	Leu	Ser								
										200											205	210	
att	gtt	tcc	ctg	gta	att	ctt	ctc	gtc	cta	atc	tca	atc	tta	ctg	tac	953							
Ile	Val	Ser	Leu	Val	Ile	Leu	Leu	Val	Leu	Ile	Ser	Ile	Leu	Leu	Tyr								
										215											220	225	
tgg	aaa	cgt	cac	cgg	aat	cag	gac	cga	gag	ccc	ttaaataagtc	acacagcacc				1006							
Trp	Lys	Arg	His	Arg	Asn	Gln	Asp	Arg	Glu	Pro													
										230											235		
ctgaaagtga	ttccctggtc	tacttgaatt	tgacacaaga	gaaaagcagg	agaaaaaggg	1066																	
gccattctcc	aaaggacctg	aaagagcaaa	agaggtggga	gcgaaagcct	taaggatccc	1126																	
acgacttttt	actgccatct	gagctactca	gtgtttgaat	cccaagagga	agtcagttta	1186																	
cctctcaggt	ctgttgtagg	acttgatttt	gtaaagcaat	gccatgttat	gtggttgaaa	1246																	
gggcactgga	cttagttagt	atcaggagca	ctgagctcac	agactgactt	gggctcctac	1306																	
tggtggggac	ctctgttagt	cactttacct	catccaaagt	ataaaggaat	tggaacaaat	1366																	
aatttaccac	atagctctaa	aacttaattt	aaaatgtaat	tccagaaaaa	aaaagggaat	1426																	

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aagcaaaggg ggaagaattg aaagagagag agaagaaaga atacagagag cttacctttt 1486
gcctttctgt tgatgttaca tctcttcttc ctatgttctt aggtctatga gtctgtttcc 1546
ccatcatttg gtatctagtc cagttcctgc ttactgcttt gctaatagct ggccttgcta 1606
gaatccttgg tttcactgct gttcttcatg tgcttctatg agatttactc caacacaaat 1666
aggactgaat ttattgtgaa gtaacattgg caatcttaac ttattcattt aacttatttt 1726
tatagctaga taaatattgt tagtcctaga caatagctca cattttttga gaagcatgcc 1786
ctccctgtcc atttgtctta taacatgacc cagccctatt ttacgtcatt ctaaattcag 1846
cctcatataa tgaaaataca ttatgaaaac agatgtttag gagatttcct gtatagcagt 1906
cagccaattc atatgctttg tctctgctgg cttctttttc catgctgtaa cttttcccaa 1966
tagcagagga ggcaaatatg agcatacaat ccctttgttc taaagatatt gttccagcta 2026
gtggaatgat gttgaatctt taataaccat aattagtgtc tttttcagta tcttctgctt 2086
tgtctgtgtc tatccagtgg cctaggaatt aaagtgtgaa ttgttttcgc tgttaaattg 2146
gatatttata tatatatata tagcaagatt ttcatgtgtt atttaattct gtattgtttc 2206
ttatatttgt agtaaaaatat tgaacaatta aaagtgttga ctccaaaaaa aaaaaaaaaa 2266

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<210> 12

<211> 262

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..23

<400> 12

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      -5                      1                      5
Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys Cys Ser Leu Gln Asn
10                      15                      20                      25
Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys Lys Lys Ala Val Ser
      30                      35                      40
Pro Glu Asn Met Val Thr Phe Ser Glu Asn His Gly Val Val Ile Gln
      45                      50                      55
Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln Leu Gly Leu Gln Asn
      60                      65                      70
Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu Asp Glu Gly Cys Tyr
      75                      80                      85
Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys Ile Ser Gly Thr Ala
90                      95                      100                      105
Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser Leu His Tyr Lys Phe
      110                      115                      120
Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala Thr Ala Arg Pro Ala
      125                      130                      135
Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly Ile Glu Asn Ser Thr
      140                      145                      150
Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser Val Thr Ser Ile Leu
      155                      160                      165
His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys Glu Val Ile Cys Gln
170                      175                      180                      185
Val Leu His Leu Gly Thr Val Thr Asp Phe Lys Gln Thr Val Asn Lys
      190                      195                      200
Gly Tyr Trp Phe Ser Val Pro Leu Leu Ser Ile Val Ser Leu Val
      205                      210                      215
Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr Trp Lys Arg His Arg

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220
Asn Gln Asp Arg Glu Pro
235

225

230

<210> 13
<211> 1597
<212> DNA
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<222> 1558..1563

<220>
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<222> 1582..1597

<400> 13
actactccag acagacggct ttggaatcca ccagctacat ccagctccct gaggcagagt 60
tgaga atg gag aga atg tta cct ctc ctg act ctg ggg ctc ttg gcg gct 110
Met Glu Arg Met Leu Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala
-20 -15 -10
ggg ttc tgc cct gct gtc ctc tgc cac cct aac agc cca ctt gac gag 158
Gly Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu
-5 1 5
gag aat ctg acc cag gag aac caa gac cga ggg aca cac gtg gac ctc 206
Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu
10 15 20
gga tta gcc tcc gcc aac gtg gac ttc gct ctc agc ctg tac aag cag 254
Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln
25 30 35 40
tta gtc ctg aag gcc cct gat aag aat gtc atc ttc tcc cca ctg agc 302
Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser
45 50 55
atc tcc acc gcc ttg gcc ttc ctg tct ctg ggg gcc cat aat acc acc 350
Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr
60 65 70
ctg aca gag att ctc aaa ggc ctc aag ttc aac ctc acg gag act tct 398
Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser
75 80 85
gag gca gaa att cac cag agc ttc cag cac ctc ctg cgc acc ctc aat 446
Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn
90 95 100
cag tcc agc gat gag ctg cag ctg agt atg gga aat gcc atg ttt gtc 494

Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val	
105 110 115 120	
aaa gag caa ctc agt ctg ctg gac agg ttc acg gag gat gcc aag agg	542
Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg	
125 130 135	
ctg tat ggc tcc gag gcc ttt gcc act gac ttt cag gac tca gct gca	590
Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala	
140 145 150	
gct aag aag ctc atc aac gac tac gtg aag aat gga act agg ggg aaa	638
Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys	
155 160 165	
atc aca gat ctg atc aag gac ctt gac tgc cag aca atg atg gtc ctg	686
Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu	
170 175 180	
gtg aat tac atc ttc ttt aaa gcc aaa tgg gag atg ccc ttt gac ccc	734
Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro	
185 190 195 200	
caa gat act cat cag tca agg ttc tac ttg agc aag aaa aag tgg gta	782
Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val	
205 210 215	
atg gtg ccc atg atg agt ttg cat cac ctg act ata cct tac ttc cgg	830
Met Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg	
220 225 230	
gac gag gag ctg tcc tgc acc gtg gtg gag ctg aag tac aca ggc aat	878
Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn	
235 240 245	
gcc agc gca ctc ttc atc ctc cct gat caa gac aag atg gag gaa gtg	926
Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val	
250 255 260	
gaa gcc atg ctg ctc cca gag acc ctg aag cgg tgg aga gac tct ctg	974
Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu	
265 270 275 280	
gag ttc aga gag ata ggt gag ctc tac ctg cca aag ttt tcc atc tgc	1022
Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser	
285 290 295	
agg gac tat aac ctg aac gac ata ctt ctc cag ctg ggc att gag gaa	1070
Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu	
300 305 310	
gcc ttc acc agc aag gct gac ctg tca ggg atc aca ggg gcc agg aac	1118
Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn	
315 320 325	
cta gca gtc tcc cag gtg gtc cat aag gct gtg ctt gat gta ttt gag	1166
Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu	
330 335 340	
gag ggc aca gaa gca tct gct gcc aca gca gtc aaa atc acc ctc ctt	1214
Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu	
345 350 355 360	
tct gca tta gtg gag aca agg acc att gtg cgt ttc aac agg ccc ttc	1262
Ser Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe	
365 370 375	
ctg atg atc att gtc cct aca gac acc cag aac atc ttc ttc atg agc	1310
Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser	
380 385 390	
aaa gtc acc aat ccc aag caa gcc tagagcttgc catcaagcag tggggctctc	1364
Lys Val Thr Asn Pro Lys Gln Ala	
395 400	

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agtaaggaac ttggaatgca agctggatgc ctgggtctct gggcacagcc tggccctgt 1424
gcaccgagtg gccatggcat gtgtggccct gtctgcttat ccttgggaagg tgacagcgat 1484
tccctgtgta gctctcacat gcacaggggc ccatggactc ttcagtctgg agggctcctgg 1544
gcctcctgac agcaataaat aatttcgttg gacacgcaaa aaaaaaaaaa aaa 1597

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<210> 14
<211> 423
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..23

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<400> 14
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      -20      -15      -10
Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
      -5      1      5
Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly
10      15      20      25
Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln Leu
      30      35      40
Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
      45      50      55
Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
      60      65      70
Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu
      75      80      85
Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln
90      95      100      105
Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
      110      115      120
Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
      125      130      135
Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
      140      145      150
Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile
      155      160      165
Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu Val
170      175      180      185
Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
      190      195      200
Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val Met
      205      210      215
Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
      220      225      230
Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
      235      240      245
Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
250      255      260      265
Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
      270      275      280
Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
      285      290      295
Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala

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300	305	310
Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu		
315	320	325
Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu Glu		
330	335	340
Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser		
	350	355
Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu		
	365	370
Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys		
	380	385
Val Thr Asn Pro Lys Gln Ala		390
395	400	

<210> 15
 <211> 1397
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..152

<220>
 <221> CDS
 <222> 153..806

<220>
 <221> 3'UTR
 <222> 807..1397

<220>
 <221> polyA_signal
 <222> 1362..1367

<220>
 <221> polyA_site
 <222> 1382..1397

<400> 15
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 cgggcgcaaa ggcaccaggg ccgcccagg gcgcctcgca gcacggcctt ggggggttctg 120
 cgggccttcg ggtgcgcgtc tcgcctctag cc atg ggg tcc gca gcg ttg gag 173
 Met Gly Ser Ala Ala Leu Glu
 1 5
 atc ctg ggc ctg gtg ctg tgc ctg gtg ggc tgg ggg ggt ctg atc ctg 221
 ile leu gly leu val leu cys leu val gly trp gly gly leu ile leu
 10 15 20
 gcg tgc ggg ctg ccc atg tgg cag gtg acc gcc ttc ctg gac cac aac 269
 ala cys gly leu pro met trp gln val thr ala phe leu asp his asn
 25 30 35
 atc gtg acg gcg cag acc acc tgg aag ggg ctg tgg atg tcg tgc gtg 317
 ile val thr ala gln thr thr trp lys gly leu trp met ser cys val
 40 45 50 55
 gtg cag agc acc ggg cac atg cag tgc aaa gtg tac gac tcg gtg ctg 365
 val gln ser thr gly his met gln cys lys val tyr asp ser val leu

```

      60      65      70
gct ctg agc acc gag gtg cag gcg gcg cgg gcg ctc acc gtg agc gcc 413
Ala Leu Ser Thr Glu Val Gln Ala Ala Arg Ala Leu Thr Val Ser Ala
      75      80      85
gtg ctg ctg gcg ttc gtt gcg ctc ttc gtg acc ctg gcg ggc gcg cag 461
Val Leu Leu Ala Phe Val Ala Leu Phe Val Thr Leu Ala Gly Ala Gln
      90      95      100
tgc acc acc tgc gtg gcc ccg ggc ccg gcc aag gcg cgt gtg gcc ctc 509
Cys Thr Thr Cys Val Ala Pro Gly Pro Ala Lys Ala Arg Val Ala Leu
      105      110      115
acg gga ggc gtg ctc tac ctg ttt tgc ggg ctg ctg gcg ctc gtg cca 557
Thr Gly Gly Val Leu Tyr Leu Phe Cys Gly Leu Leu Ala Leu Val Pro
      120      125      130      135
ctc tgc tgg ttc gcc aac att gtc gtc cgc gag ttt tac gac ccg tct 605
Leu Cys Trp Phe Ala Asn Ile Val Val Arg Glu Phe Tyr Asp Pro Ser
      140      145      150
gtg ccc gtg tgc cag aag tac gag ctg ggc gca gcg ctg tac atc ggc 653
Val Pro Val Ser Gln Lys Tyr Glu Leu Gly Ala Ala Leu Tyr Ile Gly
      155      160      165
tgg gcg gcc acc gcg ctg ctc atg gta ggc ggc tgc ctc ttg tgc tgc 701
Trp Ala Ala Thr Ala Leu Leu Met Val Gly Gly Cys Leu Leu Cys Cys
      170      175      180
ggc gcc tgg gtc tgc acc ggc cgt ccc gac ctc agc ttc ccc gtg aag 749
Gly Ala Trp Val Cys Thr Gly Arg Pro Asp Leu Ser Phe Pro Val Lys
      185      190      195
tac tca gcg ccg cgg cgg ccc acg gcc acc ggc gac aac gac aag aag 797
Tyr Ser Ala Pro Arg Arg Pro Thr Ala Thr Gly Asp Asn Asp Lys Lys
      200      205      210      215
aac tac gtc tgagggcgct gggcacggcc gggccctcc tgccagccac 846
Asn Tyr Val
gcctgcgagg cgctggataa gcctggggag ccccgcatgg accgcggcctt ccgcccggta 906
gcgcggcgcg caggcttctc ggaacgtccg gctctgcgcc ccgacgcggc tcctggatcc 966
gctcctgcct gcgcccgcag ctgaccttct cctgccacta gcccggccct gcccttaaca 1026
gacggaatga agtttccctt tctgtgcgcg gcgctgtttc cataggcaga gcgggtgtca 1086
gactgaggat ttcgcttccc ctccaagacg ctgggggtct tggctgctgc cttacttccc 1146
agaggctcct gctgacttcg gagggggcgga tgcagagccc agggccccc cgggaagatg 1206
tgtacagctg gtctttactc catcggcagg gcccagagccc agggaccagt gacttggcct 1266
ggacctcccg gtctcactcc agcatctccc caggcaaggc ttgtgggcac cggagcttga 1326
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aaaaaaaaa a 1397

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<210> 16

<211> 218

<212> PRT

<213> Homo sapiens

<400> 16

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Met Gly Ser Ala Ala Leu Glu Ile Leu Gly Leu Val Leu Cys Leu Val
1      5      10      15
Gly Trp Gly Gly Leu Ile Leu Ala Cys Gly Leu Pro Met Trp Gln Val
      20      25      30
Thr Ala Phe Leu Asp His Asn Ile Val Thr Ala Gln Thr Thr Trp Lys
      35      40      45
Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly His Met Gln Cys
      50      55      60
Lys Val Tyr Asp Ser Val Leu Ala Leu Ser Thr Glu Val Gln Ala Ala

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65		70		75		80									
Arg	Ala	Leu	Thr	Val	Ser	Ala	Val	Leu	Leu	Ala	Phe	Val	Ala	Leu	Phe
				85				90					95		
Val	Thr	Leu	Ala	Gly	Ala	Gln	Cys	Thr	Thr	Cys	Val	Ala	Pro	Gly	Pro
		100						105					110		
Ala	Lys	Ala	Arg	Val	Ala	Leu	Thr	Gly	Gly	Val	Leu	Tyr	Leu	Phe	Cys
		115						120					125		
Gly	Leu	Leu	Ala	Leu	Val	Pro	Leu	Cys	Trp	Phe	Ala	Asn	Ile	Val	Val
	130							135				140			
Arg	Glu	Phe	Tyr	Asp	Pro	Ser	Val	Pro	Val	Ser	Gln	Lys	Tyr	Glu	Leu
145					150					155					160
Gly	Ala	Ala	Leu	Tyr	Ile	Gly	Trp	Ala	Ala	Thr	Ala	Leu	Leu	Met	Val
				165						170				175	
Gly	Gly	Cys	Leu	Leu	Cys	Cys	Gly	Ala	Trp	Val	Cys	Thr	Gly	Arg	Pro
			180					185					190		
Asp	Leu	Ser	Phe	Pro	Val	Lys	Tyr	Ser	Ala	Pro	Arg	Arg	Pro	Thr	Ala
		195						200				205			
Thr	Gly	Asp	Asn	Asp	Lys	Lys	Asn	Tyr	Val						
	210						215								

<210> 17
 <211> 782
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..782

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 767..782

<400> 17	
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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg	107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly	
1 5 10 15	
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt	155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys	
20 25 30	
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg	203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu	
35 40 45	

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ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt ggc ctc tat gct gat cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgttg agttaggggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaaaaaa 772
aaaaaaaaaa 782

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<210> 18

<211> 170

<212> PRT

<213> Homo sapiens

<400> 18

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Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1 5 10 15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20 25 30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35 40 45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50 55 60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65 70 75 80
Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85 90 95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100 105 110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115 120 125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130 135 140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145 150 155 160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp

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165

170

<210> 19
 <211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

<400> 19
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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt ttg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140


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gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggaggggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactct 772
caaaaaaaaa aaaaaaa 789

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<210> 20
<211> 170
<212> PRT
<213> Homo sapiens

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<400> 20
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1 5 10 15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys Glu
20 25 30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35 40 45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50 55 60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65 70 75 80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85 90 95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100 105 110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115 120 125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130 135 140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145 150 155 160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165 170

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<210> 21
<211> 555
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..85

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<220>
<221> CDS
<222> 86..403

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<220>
<221> 3'UTR
<222> 404..555

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<220>
 <221> polyA_signal
 <222> 504..509

<220>
 <221> polyA_site
 <222> 540..555

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 agagtcaagg gcacgagcat cggccc atg cct ttc ttg gac atc cag aaa agg 112
 Met Pro Phe Leu Asp Ile Gln Lys Arg
 1 5
 ttc ggc ctt aac ata gat cga tgg ttg aca atc cag agt tgt gaa cag 160
 Phe Gly Leu Asn Ile Asp Arg Trp Leu Thr Ile Gln Ser Cys Glu Gln
 10 15 20 25
 ccc tac aag atg gct ggt cga tgc cat gct ttt gaa aaa gaa tgg ata 208
 Pro Tyr Lys Met Ala Gly Arg Cys His Ala Phe Glu Lys Glu Trp Ile
 30 35 40
 gaa tgt gca cat gga atc ggt tat act cgg gca gag aaa gag tgc aag 256
 Glu Cys Ala His Gly Ile Gly Tyr Thr Arg Ala Glu Lys Glu Cys Lys
 45 50 55
 ata gaa tat gat gat ttc gta gag tgt ttg ctt cgg cag aaa acg atg 304
 Ile Glu Tyr Asp Asp Phe Val Glu Cys Leu Leu Arg Gln Lys Thr Met
 60 65 70
 aga cgt gca ggt acc atc agg aag cag cgg gat aag ctg ata aag gaa 352
 Arg Arg Ala Gly Thr Ile Arg Lys Gln Arg Asp Lys Leu Ile Lys Glu
 75 80 85
 gga aag tac acc cct cca cct cac cac att ggc aag ggg gag cct tgg 400
 Gly Lys Tyr Thr Pro Pro Pro His His Ile Gly Lys Gly Glu Pro Trp
 90 95 100 105
 ccc tgaacagagc agctgctgat gtctggaggc tgattttcct gttctctgtt 453
 Pro
 ctccactgga aaggttggtt acgacaaacc tccttggtcaa agtgtgtataa aataaaggat 513
 tgctccatcc tatttggttct attttcaaaa aaaaaaaaaa aa 555

<210> 22
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 22
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 Trp Leu Thr Ile Gln Ser Cys Glu Gln Pro Tyr Lys Met Ala Gly Arg
 20 25 30
 Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly Ile Gly
 35 40 45
 Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp Phe Val
 50 55 60
 Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr Ile Arg
 65 70 75 80
 Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro Pro Pro
 85 90 95
 His His Ile Gly Lys Gly Glu Pro Trp Pro

100

105

<210> 23
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 415..1653

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 cgcgtcgggt ggggcgggaa taaagttttt ccaaccagc ttggggagag ggctggatgg 180
 gaaggacctt ccctgctgca gacttcatgg caggctgcac tgtgtcccct cggctccacg 240
 gctgcccccg gggcgctgct ttccgggtttt ctttctagaa tctctggtct gctgctgtgc 300
 agatggacct gccggcactg ctgtcagaag tgctacgagt ccagctgttg ccagtcaagt 360
 gaggatgaag ttgaaattct gggacctttc cctgctcaga cccctccctg gctg atg 417

Met

1

gcc agc cgg agc agt gac aag gat ggt gac tct gtc cac acg gcc agc 465
 Ala Ser Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser

5

10

15

gaa gtc ccg ctg acc cca cgg acc aat tcc ccg gat gga aga cgc tcg 513
 Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser

20

25

30

tcc tca gac aca tcc aag tct aca tac agc ctg acg cgg agg att tcg 561
 Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser

35

40

45

agt ctt gag tca aga cgt ccc agc tct cca ctc atc gat att aaa ccc 609
 Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro

50

55

60

65

atc gag ttt ggc gtt ctc agc gcc aag aag gag ccc atc caa cct tcg 657
 Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser

70

75

80

gtg ctc aga cgg acc tat aac ccc gac gac tat ttc agg aag ttc gaa 705
 Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu

85

90

95

ccc cac ctg tac tcc ctc gac tcc aac agc gac gat gtg gac tct ctg 753
 Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu

100

105

110

aca gac gag gag atc ctg tcc aag tac cag ctg ggc atg cag cac ttc 801
 Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His Phe

115	120	125	
agc act cag tac gac ctg ctg cac aac cac ctc acc gtg cgc gtg atc			849
Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val Ile			
130	135	140	145
gag gcc agg gac ctg cca cct ccc atc tcc cac gat ggc tcg cgc cag			897
Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg Gln			
150	155	160	
gac atg gcg cac tcc aac ccc tac gtc aag atc tgt ctc ctg cca gac			945
Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro Asp			
165	170	175	
cag aag aac tca aag cag acc ggg gtc aaa cgc aag acc cag aag ccc			993
Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys Pro			
180	185	190	
gtg ttt gag gag cgc tac acc ttc gag atc ccc ttc ctg gag gcc cag			1041
Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala Gln			
195	200	205	
agg agg acc ctg ctc ctg acc gtg gtg gat ttt gat aag ttc tcc cgc			1089
Arg Arg Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser Arg			
210	215	220	225
cac tgt gtc att ggg aaa gtt tct gtg cct ttg tgt gaa gtt gac ctg			1137
His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp Leu			
230	235	240	
gtc aag ggc ggg cac tgg tgg aag gcg ctg att ccc agt tct cag aat			1185
Val Lys Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln Asn			
245	250	255	
gaa gtg gag ctg ggg gag ctg ctt ctg tca ctg aat tat ctc cca agt			1233
Glu Val Glu Leu Gly Glu Leu Leu Ser Leu Asn Tyr Leu Pro Ser			
260	265	270	
gct ggc aga ctg aat gtt gat gtc att cga gcc aag caa ctt ctt cag			1281
Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln			
275	280	285	
aca gat gtg agc caa ggt tca gac ccc ttt gtg aaa atc cag ctg gtg			1329
Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val			
290	295	300	305
cat gga ctc aaa ctt gtg aaa acc aag aag acg tcc ttc tta agg ggc			1377
His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly			
310	315	320	
aca att gat cct ttc tac aat gaa tcc ttc agc ttc aaa gtt ccc caa			1425
Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln			
325	330	335	
gaa gaa ctg gaa aat gcc agc cta gtg ttt aca gtt ttc ggc cac aac			1473
Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn			
340	345	350	
atg aag agc agc aat gac ttc atc ggg agg atc gtc att ggc cag tac			1521
Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr			
355	360	365	
tct tca ggc ccc tct gag acc aac cac tgg agg cgc atg ctc aac acg			1569
Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr			
370	375	380	385
cac cgc aca gcc gtg gag cag tgg cat agc ctg agg tcc cga gct gag			1617
His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu			
390	395	400	
tgt gac cgc gtg tct cct gcc tcc ctg gag gtg acc tgagggtgc			1663
Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr			
405	410		
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aaa

1726

<210> 24

<211> 413

<212> PRT

<213> Homo sapiens

<400> 24

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      20      25      30
Ser Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile
      35      40      45
Ser Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys
      50      55      60
Pro Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro
65      70      75      80
Ser Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe
      85      90      95
Glu Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser
      100     105     110
Leu Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His
      115     120     125
Phe Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val
      130     135     140
Ile Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg
145     150     155     160
Gln Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro
      165     170     175
Asp Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys
      180     185     190
Pro Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala
      195     200     205
Gln Arg Arg Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser
      210     215     220
Arg His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp
225     230     235     240
Leu Val Lys Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln
      245     250     255
Asn Glu Val Glu Leu Gly Glu Leu Leu Ser Leu Asn Tyr Leu Pro
      260     265     270
Ser Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu
      275     280     285
Gln Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu
      290     295     300
Val His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg
305     310     315     320
Gly Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro
      325     330     335
Gln Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His
      340     345     350
Asn Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln
      355     360     365
Tyr Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn
      370     375     380

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Thr His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala
 385 390 395 400
 Glu Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr
 405 410

<210> 25
 <211> 941
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 76..339

<220>
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 <222> 340..941

<220>
 <221> polyA_signal
 <222> 903..908

<220>
 <221> polyA_site
 <222> 926..941

<400> 25
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 ccgacccccct gcacc atg gac ccc gct cgc ccc ctg ggg ctg tcg att ctg 111
 Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu
 -20 -15
 ctg ctt ttc ctg acg gag gct gca ctg ggc gat gct gct cag gag cca 159
 Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro
 -10 -5 1
 aca gga aat aac gcg gag atc tgt ctc ctg ccc cta gac tac gga ccc 207
 Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro
 5 10 15 20
 tgc cgg gcc cta ctt ctc cgt tac tac tac gac agg tac acg cag agc 255
 Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser
 25 30 35
 tgc cgc cag ttc ctg tac ggg ggc tgc gag ggc aac gcc aac aat ttc 303
 Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe
 40 45 50
 tac acc tgg gag gct tgc gac gat ctt gct gga gga tagaaaaagt 349
 Tyr Thr Trp Glu Ala Cys Asp Asp Leu Ala Gly Gly
 55 60
 tcccaaagtt tgcggctgc aagtgagtgt ggacgaccag tgtgaggggt ccacagaaaa 409
 gtattttcttt aatctaagtt ccatgacatg tgaaaaattc ttttcgggtg ggtgtcaaccg 469
 gaaccggatt gagaacaggt ttccagatga agctacttgt atgggcttct gcgcacccaaa 529
 gaaaattcca tcattttgct acagtccaaa agatggggac tgtgctctgc caatgtgact 589
 cgctattatt ttaatccaag atacagaacc tgtgatgctt tcacctatac tggctgtgga 649
 gggaatgaca ataactttgt tagcagggag gattgcaaac gtgcatgtgc aaaagctttg 709

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aaaaagaaaa agaagatgcc aaagcttcgc ttgcccagta gaatccggaa aattcggaag 769
aagcaatttt aaacattctt aatatgtcat cttgtttgtc tttatggctt atttgccttt 829
atggttgtat ctgaagaata atatgacagc atgaggaaac aaatcattgg tgatttattc 889
accagttttt attaatacaa gtcacttttt aaaaataaaa aaaaaaaaaa aa          941

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<210> 26
<211> 88
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 26
Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
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Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
      -5                      1                      5
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
      10                      15                      20
Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
      25                      30                      35                      40
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
      45                      50                      55
Ala Cys Asp Asp Leu Ala Gly Gly
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<210> 27
<211> 1894
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..20

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<220>
<221> CDS
<222> 21..1118

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<220>
<221> 3'UTR
<222> 1119..1894

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<220>
<221> polyA_signal
<222> 1858..1863

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<220>
<221> polyA_site
<222> 1879..1894

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<400> 27
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Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala

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-20										-15										
ctg	gct	ctt	ctt	tca	gcg	ttt	tcg	gcc	acc	cag	gca	cgg	aaa	ggc	ttc					101
Leu	Ala	Leu	Leu	Ser	Ala	Phe	Ser	Ala	Thr	Gln	Ala	Arg	Lys	Gly	Phe					
-10					-5					1										
tgg	gac	tac	ttc	agc	cag	acc	agc	ggg	gac	aaa	ggc	agg	gtg	gag	cag					149
Trp	Asp	Tyr	Phe	Ser	Gln	Thr	Ser	Gly	Asp	Lys	Gly	Arg	Val	Glu	Gln					
5					10					15					20					
atc	cat	cag	cag	aag	atg	gct	cgc	gag	ccc	gcg	acc	ctg	aaa	gac	agc					197
Ile	His	Gln	Gln	Lys	Met	Ala	Arg	Glu	Pro	Ala	Thr	Leu	Lys	Asp	Ser					
25					30					35										
ctt	gag	caa	gac	ctc	aac	aat	atg	aac	aag	ttc	ctg	gaa	aag	ctg	agg					245
Leu	Glu	Gln	Asp	Leu	Asn	Asn	Met	Asn	Lys	Phe	Leu	Glu	Lys	Leu	Arg					
40					45					50										
cct	ctg	agt	ggg	agc	gag	gct	cct	cgg	ctc	cca	cag	gac	ccg	gtg	ggc					293
Pro	Leu	Ser	Gly	Ser	Glu	Ala	Pro	Arg	Leu	Pro	Gln	Asp	Pro	Val	Gly					
55					60					65										
atg	cgg	cgg	cag	ctg	cag	gag	gag	ttg	gag	gag	gtg	aag	gct	cgc	ctc					341
Met	Arg	Arg	Gln	Leu	Gln	Glu	Glu	Leu	Glu	Glu	Val	Lys	Ala	Arg	Leu					
70					75					80										
cag	ccc	tac	atg	gca	gag	gcg	cac	gag	ctg	gtg	ggc	tgg	aat	ttg	gag					389
Gln	Pro	Tyr	Met	Ala	Glu	Ala	His	Glu	Leu	Val	Gly	Trp	Asn	Leu	Glu					
85					90					95					100					
ggc	ttg	cgg	cag	caa	ctg	aag	ccc	tac	acg	atg	gat	ctg	atg	gag	cag					437
Gly	Leu	Arg	Gln	Gln	Leu	Lys	Pro	Tyr	Thr	Met	Asp	Leu	Met	Glu	Gln					
105					110					115										
gtg	gcc	ctg	cgc	gtg	cag	gag	ctg	cag	gag	cag	ttg	cgc	gtg	gtg	ggg					485
Val	Ala	Leu	Arg	Val	Gln	Glu	Leu	Gln	Glu	Gln	Leu	Arg	Val	Val	Gly					
120					125					130										
gaa	gac	acc	aag	gcc	cag	ttg	ctg	ggg	ggc	gtg	gac	gag	gct	tgg	gct					533
Glu	Asp	Thr	Lys	Ala	Gln	Leu	Leu	Gly	Gly	Val	Asp	Glu	Ala	Trp	Ala					
135					140					145										
ttg	ctg	cag	gga	ctg	cag	agc	cgc	gtg	gtg	cac	cac	acc	ggc	cgc	ttc					581
Leu	Leu	Gln	Gly	Leu	Gln	Ser	Arg	Val	Val	His	His	Thr	Gly	Arg	Phe					
150					155					160										
aaa	gag	ctc	ttc	cac	cca	tac	gcc	gag	agc	ctg	gtg	agc	ggc	atc	ggg					629
Lys	Glu	Leu	Phe	His	Pro	Tyr	Ala	Glu	Ser	Leu	Val	Ser	Gly	Ile	Gly					
165					170					175					180					
cgc	cac	gtg	cag	gag	ctg	cac	cgc	agt	gtg	gct	ccg	cac	gcc	ccc	gcc					677
Arg	His	Val	Gln	Glu	Leu	His	Arg	Ser	Val	Ala	Pro	His	Ala	Pro	Ala					
185					190					195										
agc	ccc	gcg	cgc	ctc	agt	cgc	tgc	gtg	cag	gtg	ctc	tcc	cgg	aag	ctc					725
Ser	Pro	Ala	Arg	Leu	Ser	Arg	Cys	Val	Gln	Val	Leu	Ser	Arg	Lys	Leu					
200					205					210										
acg	ctc	aag	gcc	aag	gcc	ctg	cac	gca	cgc	atc	cag	cag	aac	ctg	gac					773
Thr	Leu	Lys	Ala	Lys	Ala	Leu	His	Ala	Arg	Ile	Gln	Gln	Asn	Leu	Asp					
215					220					225										
cag	ctg	cgc	gaa	gag	ctc	agc	aga	gcc	ttt	gca	ggc	act	ggg	act	gag					821
Gln	Leu	Arg	Glu	Glu	Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu					
230					235					240										
gaa	ggg	gcc	ggc	ccg	gac	ccc	cag	atg	ctc	tcc	gag	gag	gtg	cgc	cag					869
Glu	Gly	Ala	Gly	Pro	Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln					
245					250					255					260					
cga	ctt	cag	gct	ttc	cgc	cag	gac	acc	tac	ctg	cag	ata	gct	gcc	ttc					917
Arg	Leu	Gln	Ala	Phe	Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe					
265					270					275										
act	cgc	gcc	atc	gac	cag	gag	act	gag	gag	gtc	cag	cag	cag	ctg	gcg					965

Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala
 280 285 290
 cca cct cca cca ggc cac agt gcc ttc gcc cca gag ttt caa caa aca 1013
 Pro Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr
 295 300 305
 gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg 1061
 Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu
 310 315 320
 tgg gaa gac atc act cac agc ctt cat gac cag ggc cac agc cat ctg 1109
 Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu
 325 330 335 340
 ggg gac ccc tgaggatcta cctgcccagg cccattccca gcttcttgtc 1158
 Gly Asp Pro
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 aaaaaaaaaa aaaaaa 1894

<210> 28

<211> 366

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..23

<400> 28

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 -5 1 5
 Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
 10 15 20 25
 Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
 30 35 40
 Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser
 45 50 55
 Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu
 60 65 70
 Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala
 75 80 85
 Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
 90 95 100 105
 Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val
 110 115 120
 Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala

	125		130		135										
Gln	Leu	Leu	Gly	Gly	Val	Asp	Glu	Ala	Trp	Ala	Leu	Leu	Gln	Gly	Leu
	140		145		150										
Gln	Ser	Arg	Val	Val	His	His	Thr	Gly	Arg	Phe	Lys	Glu	Leu	Phe	His
	155		160		165										
Pro	Tyr	Ala	Glu	Ser	Leu	Val	Ser	Gly	Ile	Gly	Arg	His	Val	Gln	Glu
170			175		180		185								
Leu	His	Arg	Ser	Val	Ala	Pro	His	Ala	Pro	Ala	Ser	Pro	Ala	Arg	Leu
			190		195		200								
Ser	Arg	Cys	Val	Gln	Val	Leu	Ser	Arg	Lys	Leu	Thr	Leu	Lys	Ala	Lys
	205		210		215										
Ala	Leu	His	Ala	Arg	Ile	Gln	Gln	Asn	Leu	Asp	Gln	Leu	Arg	Glu	Glu
	220		225		230										
Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu	Glu	Gly	Ala	Gly	Pro
	235		240		245										
Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln	Arg	Leu	Gln	Ala	Phe
250			255		260		265								
Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	Thr	Arg	Ala	Ile	Asp
	270		275		280										
Gln	Glu	Thr	Glu	Glu	Val	Gln	Gln	Gln	Leu	Ala	Pro	Pro	Pro	Pro	Gly
	285		290		295										
His	Ser	Ala	Phe	Ala	Pro	Glu	Phe	Gln	Gln	Thr	Asp	Ser	Gly	Lys	Val
	300		305		310										
Leu	Ser	Lys	Leu	Gln	Ala	Arg	Leu	Asp	Asp	Leu	Trp	Glu	Asp	Ile	Thr
	315		320		325										
His	Ser	Leu	His	Asp	Gln	Gly	His	Ser	His	Leu	Gly	Asp	Pro		
330			335		340										

<210> 29

<211> 742

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..31

<220>

<221> CDS

<222> 32..559

<220>

<221> 3'UTR

<222> 560..742

<220>

<221> polyA_signal

<222> 702..707

<220>

<221> polyA_site

<222> 728..742

<400> 29

aatttttttg tgacttcttc agaccacttt c atg act tct gga agc aaa tgt
Met Thr Ser Gly Ser Lys Cys

52

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      1                               5
cct agt aca gac tca gga aaa gaa gaa tat att gcc acg ttc aaa gga 100
Pro Ser Thr Asp Ser Gly Lys Glu Glu Tyr Ile Ala Thr Phe Lys Gly
      10                               15                               20
tct gaa tac ttc tgc tac gac ttg tct caa aac ccc att caa agc agc 148
Ser Glu Tyr Phe Cys Tyr Asp Leu Ser Gln Asn Pro Ile Gln Ser Ser
      25                               30                               35
agt gat gaa ata act ctg tca ttt aaa acc ctt cag agg aat gga ctg 196
Ser Asp Glu Ile Thr Leu Ser Phe Lys Thr Leu Gln Arg Asn Gly Leu
      40                               45                               50                               55
atg ctt cac act ggg aaa tcg gct gat tat gtc aat ctt gcc ctg aaa 244
Met Leu His Thr Gly Lys Ser Ala Asp Tyr Val Asn Leu Ala Leu Lys
      60                               65                               70
aat gga gct gtc tct ctg gtc att aat ttg gga tca ggg gcc ttt gaa 292
Asn Gly Ala Val Ser Leu Val Ile Asn Leu Gly Ser Gly Ala Phe Glu
      75                               80                               85
gca cta gtg gag cct gtg aat gga aag ttt aat gat aat gcc tgg cat 340
Ala Leu Val Glu Pro Val Asn Gly Lys Phe Asn Asp Asn Ala Trp His
      90                               95                               100
gat gtg aaa gtc acc agg aat ctg cgt cag gtg aca ata tca gtg gat 388
Asp Val Lys Val Thr Arg Asn Leu Arg Gln Val Thr Ile Ser Val Asp
      105                               110                               115
ggg att ctt acc aca acg ggc tac acg caa gaa gat tat acc atg ctg 436
Gly Ile Leu Thr Thr Thr Gly Tyr Thr Gln Glu Asp Tyr Thr Met Leu
      120                               125                               130                               135
ggg tct gat gac ttt ttc tat gtt gga ggc agt ccc agc aca gcc gac 484
Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro Ser Thr Ala Asp
      140                               145                               150
ctt cca ggg tca cca atc cag cat gaa agc acc ttt gct gaa gac ccg 532
Leu Pro Gly Ser Pro Ile Gln His Glu Ser Thr Phe Ala Glu Asp Pro
      155                               160                               165
atg ttc cag agt caa acg gca caa ctt taaattcaat attctactat 579
Met Phe Gln Ser Gln Thr Ala Gln Leu
      170                               175
tgtttatgta ggattggggg agggaaacag ctcatagatc attatgaagg aattagggttc 639
ctcttcttta ttagtctgta agtaatttac attgagatt tgtgtggaca gttgatatta 699
gctataaaaag aaagtcaaac aaaaagagaa aaaaaaaaaa aaa 742

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<210> 30

<211> 176

<212> PRT

<213> Homo sapiens

<400> 30

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Met Thr Ser Gly Ser Lys Cys Pro Ser Thr Asp Ser Gly Lys Glu Glu
1                               5                               10                               15
Tyr Ile Ala Thr Phe Lys Gly Ser Glu Tyr Phe Cys Tyr Asp Leu Ser
      20                               25                               30
Gln Asn Pro Ile Gln Ser Ser Ser Asp Glu Ile Thr Leu Ser Phe Lys
      35                               40                               45
Thr Leu Gln Arg Asn Gly Leu Met Leu His Thr Gly Lys Ser Ala Asp
      50                               55                               60
Tyr Val Asn Leu Ala Leu Lys Asn Gly Ala Val Ser Leu Val Ile Asn
      65                               70                               75                               80
Leu Gly Ser Gly Ala Phe Glu Ala Leu Val Glu Pro Val Asn Gly Lys
      85                               90                               95

```

```

Phe Asn Asp Asn Ala Trp His Asp Val Lys Val Thr Arg Asn Leu Arg
      100      105      110
Gln Val Thr Ile Ser Val Asp Gly Ile Leu Thr Thr Thr Gly Tyr Thr
      115      120      125
Gln Glu Asp Tyr Thr Met Leu Gly Ser Asp Asp Phe Phe Tyr Val Gly
      130      135      140
Gly Ser Pro Ser Thr Ala Asp Leu Pro Gly Ser Pro Ile Gln His Glu
145      150      155      160
Ser Thr Phe Ala Glu Asp Pro Met Phe Gln Ser Gln Thr Ala Gln Leu
      165      170      175

```

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<210> 31
<211> 1766
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..3

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<220>
<221> CDS
<222> 4..1533

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<220>
<221> 3'UTR
<222> 1534..1766

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<220>
<221> polyA_signal
<222> 1709..1714

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<220>
<221> polyA_site
<222> 1744..1766

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<400> 31
aag atg gcg gcg gag ctg gtg gag gcc aaa aac atg gtg atg agt ttt      48
      Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe
      1      5      10
cga gtc tcc gac ctt cag atg ctc ctg ggt ttc gtg ggc cgg agt aag      96
Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys
      20      25      30
agt gga ctg aag cac gag ctc gtc acc agg gcc ctc cag ctg gtg cag      144
Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln
      35      40      45
ttt gac tgt acc cct gag ctg ttc aag aag atc aag gag ctg tac gag      192
Phe Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu
      50      55      60
acc cgc tac gcc aag aag aac tcg gag cct gcc cca cag ccg cac cgg      240
Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg
      65      70      75
ccc ctg gac ccc ctg acc atg cac tcc acc tac gac cgg gcc ggc gct      288
Pro Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala
      80      85      90      95
gtg ccc agg act ccg ctg gca ggc ccc aat att gac tac ccc gtg ctc      336

```

Val	Pro	Arg	Thr	Pro	Leu	Ala	Gly	Pro	Asn	Ile	Asp	Tyr	Pro	Val	Leu	
				100					105					110		
tac	gga	aag	tac	tta	aac	gga	ctg	gga	cgg	ttg	ccc	gcc	aag	acc	ctc	384
Tyr	Gly	Lys	Tyr	Leu	Asn	Gly	Leu	Gly	Arg	Leu	Pro	Ala	Lys	Thr	Leu	
				115				120					125			
aag	cca	gaa	gtc	cgc	ctg	gtg	aag	ctg	ccg	ttc	ttt	aat	atg	ctg	gac	432
Lys	Pro	Glu	Val	Arg	Leu	Val	Lys	Leu	Pro	Phe	Phe	Asn	Met	Leu	Asp	
		130					135					140				
gag	ctg	ctg	aag	ccc	acc	gaa	tta	gtc	cca	cag	aac	aac	gag	aag	ctt	480
Glu	Leu	Leu	Lys	Pro	Thr	Glu	Leu	Val	Pro	Gln	Asn	Asn	Glu	Lys	Leu	
	145					150				155						
cag	gag	agc	ccg	tgc	atc	ttc	gca	ttg	acg	cca	aga	cag	gtg	gag	ttg	528
Gln	Glu	Ser	Pro	Cys	Ile	Phe	Ala	Leu	Thr	Pro	Arg	Gln	Val	Glu	Leu	
160				165					170				175			
atc	cgg	aac	tcc	agg	gaa	ctg	cag	ccc	gga	gtt	aaa	gcc	gtg	cag	gtc	576
Ile	Arg	Asn	Ser	Arg	Glu	Leu	Gln	Pro	Gly	Val	Lys	Ala	Val	Gln	Val	
				180				185				190				
gtc	ctg	aga	atc	tgt	tac	tca	gac	acc	agc	tgc	cct	cag	gag	gac	cag	624
Val	Leu	Arg	Ile	Cys	Tyr	Ser	Asp	Thr	Ser	Cys	Pro	Gln	Glu	Asp	Gln	
				195				200				205				
tac	ccg	ccc	aac	atc	gct	gtg	aag	gtc	aac	cac	agc	tac	tgc	tcc	gtc	672
Tyr	Pro	Pro	Asn	Ile	Ala	Val	Lys	Val	Asn	His	Ser	Tyr	Cys	Ser	Val	
		210				215					220					
ccg	ggc	tac	tac	ccc	tcc	aat	aag	ccc	ggg	gtg	gag	ccc	aag	agg	ccg	720
Pro	Gly	Tyr	Tyr	Pro	Ser	Asn	Lys	Pro	Gly	Val	Glu	Pro	Lys	Arg	Pro	
	225				230				235							
tgc	cgc	ccc	atc	aac	ctc	acc	cac	ctc	atg	tac	ctt	tcc	tcg	gcc	acc	768
Cys	Arg	Pro	Ile	Asn	Leu	Thr	His	Leu	Met	Tyr	Leu	Ser	Ser	Ala	Thr	
240				245				250				255				
aac	cgc	atc	act	gtc	acc	tgg	ggg	aac	tac	ggc	aag	agc	tac	tcg	gtg	816
Asn	Arg	Ile	Thr	Val	Thr	Trp	Gly	Asn	Tyr	Gly	Lys	Ser	Tyr	Ser	Val	
			260				265				270					
gcc	ctg	tac	ctg	gtg	cgg	cag	ctg	acc	tca	tcg	gag	ctg	ctg	cag	agg	864
Ala	Leu	Tyr	Leu	Val	Arg	Gln	Leu	Thr	Ser	Ser	Glu	Leu	Leu	Gln	Arg	
		275				280					285					
ctg	aag	acc	att	ggg	gta	aag	cac	ccg	gag	ctg	tgc	aag	gca	ctg	gtc	912
Leu	Lys	Thr	Ile	Gly	Val	Lys	His	Pro	Glu	Leu	Cys	Lys	Ala	Leu	Val	
		290				295					300					
aag	gag	aag	ctg	cgc	ctt	gat	cct	gac	agc	gag	atc	gcc	acc	acc	ggc	960
Lys	Glu	Lys	Leu	Arg	Leu	Asp	Pro	Asp	Ser	Glu	Ile	Ala	Thr	Thr	Gly	
	305				310					315						
gtg	cgg	gtg	tcc	ctc	atc	tgt	ccg	ctg	gtg	aag	atg	cgg	ctc	tcc	gtg	1008
Val	Arg	Val	Ser	Leu	Ile	Cys	Pro	Leu	Val	Lys	Met	Arg	Leu	Ser	Val	
320				325					330					335		
ccc	tgc	cgg	gca	gag	acc	tgc	gcc	cac	ctg	cag	tgc	ttc	gac	gcc	gtc	1056
Pro	Cys	Arg	Ala	Glu	Thr	Cys	Ala	His	Leu	Gln	Cys	Phe	Asp	Ala	Val	
			340					345				350				
ttc	tac	ctg	cag	atg	aac	gag	aag	aag	ccc	acc	tgg	atg	tgc	ccc	gtg	1104
Phe	Tyr	Leu	Gln	Met	Asn	Glu	Lys	Lys	Pro	Thr	Trp	Met	Cys	Pro	Val	
		355				360					365					
tgc	gac	aag	cca	gcc	ccc	tac	gac	cag	ctc	atc	atc	gac	ggg	ctc	ctc	1152
Cys	Asp	Lys	Pro	Ala	Pro	Tyr	Asp	Gln	Leu	Ile	Ile	Asp	Gly	Leu	Leu	
		370				375					380					
tcg	aag	atc	ctg	agc	gag	tgt	gag	gac	gcc	gac	gag	atc	gag	tac	ctg	1200
Ser	Lys	Ile	Leu	Ser	Glu	Cys	Glu	Asp	Ala	Asp	Glu	Ile	Glu	Tyr	Leu	
	385					390					395					

```

gtg gac ggc tcg tgg tgc ccg atc cgc gcc gaa aag gag ctc agc tgc 1248
Val Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys
400 405 410 415
agc ccg cag ggc gcc atc ctc gtg ctg ggc ccc tcg gac gcc aat ggg 1296
Ser Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly
420 425 430
ctc ctg ccc gcc ccc agc gtc aac ggg agc ggt gcc ctg ggc agc acg 1344
Leu Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr
435 440 445
ggt ggc ggc ggc ccg gtg ggc agc atg gag aat ggg aag ccg ggc gcc 1392
Gly Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala
450 455 460
gat gtg gtg gac ctc acg ctg gac agc tca tcg tcc tcg gag gat gag 1440
Asp Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu
465 470 475
gag gag gag gaa gag gag gag gaa gac gag gac gaa gag ggg ccc cgg 1488
Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg
480 485 490 495
ccc aag cgc cgc tgc ccc ttc cag aag ggc ctg gtg ccg gcc tgc 1533
Pro Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys
500 505 510
tgaccccggc cgcacacttg actttccttg tgctcaccac gcagaggggc acgggccagc 1593
ctcgggcgca gagggaggag tgacctttct ttttcctttt attgtcgttc gttttgtttt 1653
tccacctttt tgcttggtc ctggcacctg tacctctgga ctctctatc gggggattaa 1713
aaaaaaaaagt aaaatgacaa aaaaagatac aaaaaagaaa aaaaaaaaaaaa aaa 1766

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<210> 32

<211> 510

<212> PRT

<213> Homo sapiens

<400> 32

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Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg
1 5 10 15
Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
20 25 30
Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe
35 40 45
Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr
50 55 60
Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro
65 70 75 80
Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala Val
85 90 95
Pro Arg Thr Pro Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu Tyr
100 105 110
Gly Lys Tyr Leu Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu Lys
115 120 125
Pro Glu Val Arg Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp Glu
130 135 140
Leu Leu Lys Pro Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu Gln
145 150 155 160
Glu Ser Pro Cys Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu Ile
165 170 175
Arg Asn Ser Arg Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val Val
180 185 190

```

```

Leu Arg Ile Cys Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln Tyr
      195                200                205
Pro Pro Asn Ile Ala Val Lys Val Asn His Ser Tyr Cys Ser Val Pro
      210                215                220
Gly Tyr Tyr Pro Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro Cys
225                230                235                240
Arg Pro Ile Asn Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr Asn
      245                250                255
Arg Ile Thr Val Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val Ala
      260                265                270
Leu Tyr Leu Val Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg Leu
      275                280                285
Lys Thr Ile Gly Val Lys His Pro Glu Leu Cys Lys Ala Leu Val Lys
      290                295                300
Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly Val
305                310                315                320
Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val Pro
      325                330                335
Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val Phe
      340                345                350
Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val Cys
      355                360                365
Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu Ser
      370                375                380
Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu Val
385                390                395                400
Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys Ser
      405                410                415
Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly Leu
      420                425                430
Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr Gly
      435                440                445
Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala Asp
      450                455                460
Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu Glu
465                470                475                480
Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg Pro
      485                490                495
Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys
      500                505                510

```

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<210> 33
<211> 877
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..10

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<220>
<221> CDS
<222> 11..802

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<220>
<221> 3'UTR

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<222> 803..877

<220>

<221> polyA_signal

<222> 836..841

<220>

<221> polyA_site

<222> 862..877

<400> 33

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atctgccacg atg ttg ctg ctc agc ctg acc cta agc ctg gtt ctc ctc      49
      Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu
                -15                      -10
ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc      97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser
-5                      1                      5                      10
ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg      145
Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp
                15                      20                      25
ccc tgg cag gtg tcc ctg cag gac agc agc gac ttc cac ttc tgc ggt      193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly
                30                      35                      40
ggg tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat      241
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn
                45                      50                      55
gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca      289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
60                      65                      70                      75
tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca      337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr
                80                      85                      90
cac cct agc tgg aac tct acc acc atg aac aat gac gtg acg ctg ctg      385
His Pro Ser Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu
                95                      100                      105
aag ctc gcc tcg cca gcc cag tac aca aca cgc atc tcg cca gtt tgc      433
Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys
                110                      115                      120
ctg gca tcc tca aac gag gct ctg act gaa ggc ctc acg tgt gtc acc      481
Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr
                125                      130                      135
acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg aca cca gca cgt      529
Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala Arg
140                      145                      150                      155
ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag tgc cgg cag      577
Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln
                160                      165                      170
tac tgg ggc tca agt atc act gac tcc atg atc tgt gca ggt ggc gca      625
Tyr Trp Gly Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala
                175                      180                      185
ggg gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc cag      673
Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln
                190                      195                      200
aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa      721
Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys
205                      210                      215

```



```

aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc      769
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe
220                225                230                235
agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc 822
Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn
                240                245
cccagctcaa ccattaaag acccaggccc tgtcccatca aaaaaaaaaa aaaaa      877

```

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<210> 34
<211> 264
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..18

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<400> 34
Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser
      -15                -10                -5
Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln
      1                5                10
Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
15                20                25                30
Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly Gly Ser Leu
      35                40                45
Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
      50                55                60
Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
      65                70                75
Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
      80                85                90
Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
95                100                105                110
Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
      115                120                125
Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
      130                135                140
Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln
      145                150                155
Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
      160                165                170
Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala Gly Ala Ser
175                180                185                190
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
      195                200                205
Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
      210                215                220
Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
      225                230                235
Ile Asn Gln Val Ile Ala Tyr Asn
      240                245

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<210> 35
<211> 1728
<212> DNA

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<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..37

<220>

<221> CDS

<222> 38..1378

<220>

<221> 3'UTR

<222> 1379..1728

<220>

<221> polyA_site

<222> 1713..1728

<400> 35

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atcatctgca cagctggggc ccctgggagg agacgcc atg atc ccc acc ttc acg      55
                                Met Ile Pro Thr Phe Thr
                                -20
gct ctg ctc tgc ctc ggg ctg agt ctg ggc ccc agg acc cac atg cag      103
Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Met Gln
                                -15                    -10                    -5
gca ggg ccc ctc ccc aaa ccc acc ctc tgg gct gag cca ggc tct gtg      151
Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val
    1                    5                    10                    15
atc agc tgg ggg aac tct gtg acc atc tgg tgt cag ggg acc ctg gag      199
Ile Ser Trp Gly Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu
                                20                    25                    30
gct cgg gag tac cgt ctg gat aaa gag gaa agc cca gca ccc tgg gac      247
Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp
                                35                    40                    45
aga cag aac cca ctg gag ccc aag aac aag gcc aga ttc tcc atc cca      295
Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro
                                50                    55                    60
tcc atg aca gag gac tat gca ggg aga tac cgc tgt tac tat cgc agc      343
Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser
    65                    70                    75
cct gta ggc tgg tca cag ccc agt gac ccc ctg gag ctg gtg atg aca      391
Pro Val Gly Trp Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr
    80                    85                    90                    95
gga gcc tac agt aaa ccc acc ctt tca gcc ctg ccg agt cct ctt gtg      439
Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val
                                100                    105                    110
acc tca gaa aag agc gtg acc ctg ctg tgt cag tca cgg agc cca atg      487
Thr Ser Glu Lys Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met
                                115                    120                    125
gac act ttc ctt ctg atc aag gag cgg gca gcc cat ccc cta ctg cat      535
Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His
                                130                    135                    140
ctg aga tca gag cac gga gct cag cag cac cag gct gaa ttc ccc atg      583
Leu Arg Ser Glu His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met
                                145                    150                    155
agt cct gtg acc tca gtg cac ggg ggg acc tac agg tgc ttc agc tca      631

```

Ser	Pro	Val	Thr	Ser	Val	His	Gly	Gly	Thr	Tyr	Arg	Cys	Phe	Ser	Ser		
160					165					170					175		
cac	ggc	ttc	tcc	cac	tac	ctg	ctg	tca	cac	ccc	agt	gac	ccc	ctg	gag	679	
His	Gly	Phe	Ser	His	Tyr	Leu	Leu	Ser	His	Pro	Ser	Asp	Pro	Leu	Glu		
				180					185					190			
ctc	ata	gtc	tca	gga	tcc	ttg	gag	gat	ccc	agg	ccc	tca	ccc	aca	agg	727	
Leu	Ile	Val	Ser	Gly	Ser	Leu	Glu	Asp	Pro	Arg	Pro	Ser	Pro	Thr	Arg		
				195					200					205			
tcc	gtc	tca	aca	gct	gca	ggc	cct	gag	gac	cag	ccc	ctc	atg	cct	aca	775	
Ser	Val	Ser	Thr	Ala	Ala	Gly	Pro	Glu	Asp	Gln	Pro	Leu	Met	Pro	Thr		
				210					215					220			
ggg	tca	gtc	ccc	cac	agt	ggt	ctg	aga	agg	cac	tgg	gag	gta	ctg	atc	823	
Gly	Ser	Val	Pro	His	Ser	Gly	Leu	Arg	Arg	His	Trp	Glu	Val	Leu	Ile		
				225					230					235			
ggg	gtc	ttg	gtg	gtc	tcc	atc	ctg	ctt	ctc	tcc	ctc	ctc	ctc	ttc	ctc	871	
Gly	Val	Leu	Val	Val	Ser	Ile	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Phe	Leu		
240					245					250					255		
ctc	ctc	caa	cac	tgg	cgt	cag	gga	aaa	cac	agg	aca	ttg	gcc	cag	aga	919	
Leu	Leu	Gln	His	Trp	Arg	Gln	Gly	Lys	His	Arg	Thr	Leu	Ala	Gln	Arg		
				260						265				270			
cag	gct	gat	ttc	caa	cgt	cct	cca	ggg	gct	gcc	gag	cca	gag	ccc	aag	967	
Gln	Ala	Asp	Phe	Gln	Arg	Pro	Pro	Gly	Ala	Ala	Glu	Pro	Glu	Pro	Lys		
				275					280					285			
gac	ggg	ggc	cta	cag	agg	agg	tcc	agc	cca	gct	gct	gac	gtc	cag	gga	1015	
Asp	Gly	Gly	Leu	Gln	Arg	Arg	Ser	Ser	Pro	Ala	Ala	Asp	Val	Gln	Gly		
				290				295					300				
gaa	aac	ttc	tgt	gct	gcc	gtg	aag	gac	aca	cag	cct	gag	gac	ggg	gtg	1063	
Glu	Asn	Phe	Cys	Ala	Ala	Val	Lys	Asp	Thr	Gln	Pro	Glu	Asp	Gly	Val		
				305						310				315			
gaa	atg	gac	act	cgg	agc	cca	cac	gat	gaa	gac	ccc	cag	gca	gtg	acg	1111	
Glu	Met	Asp	Thr	Arg	Ser	Pro	His	Asp	Glu	Asp	Pro	Gln	Ala	Val	Thr		
				320						325				330			
tat	gcc	aag	gtg	aaa	cac	tcc	aga	cct	agg	aga	gaa	atg	gcc	tct	cct	1159	
Tyr	Ala	Lys	Val	Lys	His	Ser	Arg	Pro	Arg	Arg	Glu	Met	Ala	Ser	Pro		
				340						345				350			
ccc	tcc	cca	ctg	tct	ggg	gaa	ttc	ctg	gac	aca	aag	gac	aga	cag	gca	1207	
Pro	Ser	Pro	Leu	Ser	Gly	Glu	Phe	Leu	Asp	Thr	Lys	Asp	Arg	Gln	Ala		
				355					360					365			
gaa	gag	gac	aga	cag	atg	gac	act	gag	gct	gct	gca	tct	gaa	gcc	ccc	1255	
Glu	Glu	Asp	Arg	Gln	Met	Asp	Thr	Glu	Ala	Ala	Ala	Ser	Glu	Ala	Pro		
				370					375					380			
cag	gat	gtg	acc	tac	gcc	cag	ctg	cac	agc	ttt	acc	ctc	aga	cag	aag	1303	
Gln	Asp	Val	Thr	Tyr	Ala	Gln	Leu	His	Ser	Phe	Thr	Leu	Arg	Gln	Lys		
				385					390					395			
gca	act	gag	cct	cct	cca	tcc	cag	gaa	ggg	gcc	tct	cca	gct	gag	ccc	1351	
Ala	Thr	Glu	Pro	Pro	Pro	Ser	Gln	Glu	Gly	Ala	Ser	Pro	Ala	Glu	Pro		
				400					405					410			
agt	gtc	tat	gcc	act	ctg	gcc	atc	cac	taatccaggg	gggacccaga						1398	
Ser	Val	Tyr	Ala	Thr	Leu	Ala	Ile	His									
				420													
ccccacaagc	catggagact	caggacccca	gaaggcatgg	aagctgcctc	cagtagacat	1458											
cactgaaccc	cagccagccc	agacccctga	cacagaccac	tagaagattc	cggaacggtt	1518											
gggagtcacc	tgattctgca	aagataaata	atatccctgc	attatcaaaa	ttaaagtagca	1578											
gacctctcaa	ttcacaatga	gttaactgat	aaaacaaaac	agaagtcaga	caatgtttta	1638											
aattgaatga	tcatgtaaat	attacacatc	aaaccaatga	catgggaaaa	tgggagcttc	1698											
taatgaggac	aaacaaaaaa	aaaaaaaaaa				1728											

<210> 36
 <211> 447
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..23

<400> 36
 Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
 -20 -15 -10
 Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
 -5 1 5
 Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp
 10 15 20 25
 Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
 30 35 40
 Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
 45 50 55
 Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
 60 65 70
 Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
 75 80 85
 Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala
 90 95 100 105
 Leu Pro Ser Pro Leu Val Thr Ser Glu Lys Ser Val Thr Leu Leu Cys
 110 115 120
 Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
 125 130 135
 Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His
 140 145 150
 Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
 155 160 165
 Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
 170 175 180 185
 Pro Ser Asp Pro Leu Glu Leu Ile Val Ser Gly Ser Leu Glu Asp Pro
 190 195 200
 Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
 205 210 215
 Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
 220 225 230
 His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
 235 240 245
 Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His
 250 255 260 265
 Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
 270 275 280
 Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro
 285 290 295
 Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asp Thr
 300 305 310
 Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu
 315 320 325
 Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro Arg

```

330          335          340          345
Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp
          350          355          360
Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala
          365          370          375
Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser
          380          385          390
Phe Thr Leu Arg Gln Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly
          395          400          405
Ala Ser Pro Ala Glu Pro Ser Val Tyr Ala Thr Leu Ala Ile His
410          415          420

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<210> 37
<211> 1757
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..329

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<220>
<221> CDS
<222> 330..1478

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<220>
<221> 3'UTR
<222> 1479..1757

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<220>
<221> polyA_signal
<222> 1722..1727

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<220>
<221> polyA_site
<222> 1742..1757

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<400> 37
atttagttga agctgcaggg gagtgaggga gaggaggata ggaagcagga aagcgggaga 60
gctcgagggga caaggggggct cgggtgtgttt acaccaggca cgggctacga gcgtccatcc 120
cgccccctgg cttgcgctcc cgaagaggag agcaaggctg ttctgggac cggccgtcgt 180
gcggaagag gcttgtctgt cggggttgcc ggaaccagga gaaccagag ggaaaccgag 240
gcaaaggagc ggcgcgtttt actagagaga gcgcgagcgg aagaggcgag agcaggagcg 300
cgcgaggggag catcgagcgc agcggagac atg agg acc tac tgg ctg cac agc 353
                                Met Arg Thr Tyr Trp Leu His Ser
                                -20
gtc tgg gtg ctg ggc ttt ttc ctg tcc ctc ttc tca ttg caa gga ctg 401
Val Trp Val Leu Gly Phe Phe Leu Ser Leu Phe Ser Leu Gln Gly Leu
-15          -10          -5          1
cct gtt cgc agc gtg gat ttt aac cga ggc acg gac aac atc acc gtg 449
Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val
          5          10          15
agg cag ggg gac aca gcc atc ctc agg tgc gtt gta gaa gac aag aac 497
Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn
          20          25          30
tca aag gtg gcc tgg ttg aac cgt tct ggc atc att ttt gct gga cat 545

```

Ser	Lys	Val	Ala	Trp	Leu	Asn	Arg	Ser	Gly	Ile	Ile	Phe	Ala	Gly	His	
35						40					45					
gac	aag	tgg	tct	ctg	gac	cca	cgg	gtt	gag	ctg	gag	aaa	cgc	cat	tct	593
Asp	Lys	Trp	Ser	Leu	Asp	Pro	Arg	Val	Glu	Leu	Glu	Lys	Arg	His	Ser	
50					55					60					65	
ctg	gaa	tac	agc	ctc	cga	atc	cag	aag	gtg	gat	gtc	tat	gat	gag	ggg	641
Leu	Glu	Tyr	Ser	Leu	Arg	Ile	Gln	Lys	Val	Asp	Val	Tyr	Asp	Glu	Gly	
				70					75					80		
tcc	tac	act	tgc	tca	gtt	cag	aca	cag	cat	gag	ccc	aag	acc	tcc	caa	689
Ser	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Gln	His	Glu	Pro	Lys	Thr	Ser	Gln	
			85					90					95			
gtt	tac	ttg	atc	gta	caa	gtc	cca	cca	aag	atc	tcc	aat	atc	tcc	tcg	737
Val	Tyr	Leu	Ile	Val	Gln	Val	Pro	Lys	Ile	Ser	Asn	Ile	Ser	Ser		
		100					105					110				
gat	gtc	act	gtg	aat	gag	ggc	agc	aac	gtg	act	ctg	gtc	tgc	atg	gcc	785
Asp	Val	Thr	Val	Asn	Glu	Gly	Ser	Asn	Val	Thr	Leu	Val	Cys	Met	Ala	
		115				120						125				
aat	ggc	cgt	cct	gaa	cct	gtt	atc	acc	tgg	aga	cac	ctt	aca	cca	act	833
Asn	Gly	Arg	Pro	Glu	Pro	Val	Ile	Thr	Trp	Arg	His	Leu	Thr	Pro	Thr	
130					135					140					145	
gga	agg	gaa	ttt	gaa	gga	gaa	gaa	gaa	tat	ctg	gag	atc	ctt	ggc	atc	881
Gly	Arg	Glu	Phe	Glu	Gly	Glu	Glu	Glu	Tyr	Leu	Glu	Ile	Leu	Gly	Ile	
			150						155					160		
acc	agg	gag	cag	tca	ggc	aaa	tat	gag	tgc	aaa	gct	gcc	aac	gag	gtc	929
Thr	Arg	Glu	Gln	Ser	Gly	Lys	Tyr	Glu	Cys	Lys	Ala	Ala	Asn	Glu	Val	
			165					170					175			
tcc	tcg	gcg	gat	gtc	aaa	caa	gtc	aag	gtc	act	gtg	aac	tat	cct	ccc	977
Ser	Ser	Ala	Asp	Val	Lys	Gln	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	
		180						185					190			
act	atc	aca	gaa	tcc	aag	agc	aat	gaa	gcc	acc	aca	gga	cga	caa	gct	1025
Thr	Ile	Thr	Glu	Ser	Lys	Ser	Asn	Glu	Ala	Thr	Thr	Gly	Arg	Gln	Ala	
		195					200						205			
tca	ctc	aaa	tgt	gag	gcc	tcg	gca	gtg	cct	gca	cct	gac	ttt	gag	tgg	1073
Ser	Leu	Lys	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ala	Pro	Asp	Phe	Glu	Trp	
210					215					220					225	
tac	cgg	gat	gac	act	agg	ata	aat	agt	gcc	aat	ggc	ctt	gag	att	aag	1121
Tyr	Arg	Asp	Asp	Thr	Arg	Ile	Asn	Ser	Ala	Asn	Gly	Leu	Glu	Ile	Lys	
				230					235					240		
agc	acg	gag	ggc	cag	tct	tcc	ctg	acg	gtg	acc	aac	gtc	act	gag	gag	1169
Ser	Thr	Glu	Gly	Gln	Ser	Ser	Leu	Thr	Val	Thr	Asn	Val	Thr	Glu	Glu	
			245					250					255			
cac	tac	ggc	aac	tac	acc	tgt	gtg	gct	gcc	aac	aag	ctg	ggg	gtc	acc	1217
His	Tyr	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ala	Asn	Lys	Leu	Gly	Val	Thr	
		260					265						270			
aat	gcc	agc	cta	gtc	ctt	ttc	aaa	cgt	gtt	tta	ccc	aca	atc	ccc	cac	1265
Asn	Ala	Ser	Leu	Val	Leu	Phe	Lys	Arg	Val	Leu	Pro	Thr	Ile	Pro	His	
		275				280							285			
ccc	att	caa	gaa	att	ggg	acc	acc	gtg	cac	ttc	aag	caa	aaa	ggc	atc	1313
Pro	Ile	Gln	Glu	Ile	Gly	Thr	Thr	Val	His	Phe	Lys	Gln	Lys	Gly	Ile	
290					295					300					305	
ttc	ctc	tct	gag	tct	cag	agg	ggg	gag	aca	acc	aag	atc	act	ctc	aac	1361
Phe	Leu	Ser	Glu	Ser	Gln	Arg	Gly	Glu	Thr	Thr	Lys	Ile	Thr	Leu	Asn	
				310					315					320		
tgt	gga	aat	cta	ttc	ttg	cgg	aac	tta	cat	ccc	acc	agt	gat	caa	gag	1409
Cys	Gly	Asn	Leu	Phe	Leu	Arg	Asn	Leu	His	Pro	Thr	Ser	Asp	Gln	Glu	
			325					330						335		

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cca cag aga tta tgg aca ctt tgt tgc tta ctc cca aga aag ggc cag 1457
Pro Gln Arg Leu Trp Thr Leu Cys Cys Leu Leu Pro Arg Lys Gly Gln
      340                      345                      350
cac cgt att tat ggc cag tgc tagaagggtcc tcaactgaagg caacagggaa 1508
His Arg Ile Tyr Gly Gln Cys
      355                      360
gaggcagcca tgaatatata cttggaaaaca ggatcatttg aggccttcaa gaaggcataa 1568
aatattgtcc ctttcagcct ttcttttctt ctcaatgccg cgattaccaa ttatgtttta 1628
atcttaagtg gctagtgtta tatgtgatac attatgcctt tgatatgtgg ttgaaaaaat 1688
aaggcatagc attgtttttt atttcaaaaga caaaataaac tgccagtgtc accaaaaaaa 1748
aaaaaaaaa 1757

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<210> 38

<211> 383

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..23

<400> 38

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Met Arg Thr Tyr Trp Leu His Ser Val Trp Val Leu Gly Phe Phe Leu
      -20                      -15                      -10
Ser Leu Phe Ser Leu Gln Gly Leu Pro Val Arg Ser Val Asp Phe Asn
      -5                      1                      5
Arg Gly Thr Asp Asn Ile Thr Val Arg Gln Gly Asp Thr Ala Ile Leu
10      15      20      25
Arg Cys Val Val Glu Asp Lys Asn Ser Lys Val Ala Trp Leu Asn Arg
      30      35      40
Ser Gly Ile Ile Phe Ala Gly His Asp Lys Trp Ser Leu Asp Pro Arg
      45      50      55
Val Glu Leu Glu Lys Arg His Ser Leu Glu Tyr Ser Leu Arg Ile Gln
      60      65      70
Lys Val Asp Val Tyr Asp Glu Gly Ser Tyr Thr Cys Ser Val Gln Thr
      75      80      85
Gln His Glu Pro Lys Thr Ser Gln Val Tyr Leu Ile Val Gln Val Pro
90      95      100      105
Pro Lys Ile Ser Asn Ile Ser Ser Asp Val Thr Val Asn Glu Gly Ser
      110      115      120
Asn Val Thr Leu Val Cys Met Ala Asn Gly Arg Pro Glu Pro Val Ile
      125      130      135
Thr Trp Arg His Leu Thr Pro Thr Gly Arg Glu Phe Glu Gly Glu Glu
      140      145      150
Glu Tyr Leu Glu Ile Leu Gly Ile Thr Arg Glu Gln Ser Gly Lys Tyr
      155      160      165
Glu Cys Lys Ala Ala Asn Glu Val Ser Ser Ala Asp Val Lys Gln Val
170      175      180      185
Lys Val Thr Val Asn Tyr Pro Pro Thr Ile Thr Glu Ser Lys Ser Asn
      190      195      200
Glu Ala Thr Thr Gly Arg Gln Ala Ser Leu Lys Cys Glu Ala Ser Ala
      205      210      215
Val Pro Ala Pro Asp Phe Glu Trp Tyr Arg Asp Asp Thr Arg Ile Asn
      220      225      230
Ser Ala Asn Gly Leu Glu Ile Lys Ser Thr Glu Gly Gln Ser Ser Leu
      235      240      245

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Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr Thr Cys Val
250                255                260                265
Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val Leu Phe Lys
                270                275                280
Arg Val Leu Pro Thr Ile Pro His Pro Ile Gln Glu Ile Gly Thr Thr
                285                290                295
Val His Phe Lys Gln Lys Gly Ile Phe Leu Ser Glu Ser Gln Arg Gly
                300                305                310
Glu Thr Thr Lys Ile Thr Leu Asn Cys Gly Asn Leu Phe Leu Arg Asn
                315                320                325
Leu His Pro Thr Ser Asp Gln Glu Pro Gln Arg Leu Trp Thr Leu Cys
330                335                340                345
Cys Leu Leu Pro Arg Lys Gly Gln His Arg Ile Tyr Gly Gln Cys
                350                355                360

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<210> 39
<211> 2818
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..80

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<220>
<221> CDS
<222> 81..1517

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<220>
<221> 3'UTR
<222> 1518..2818

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<220>
<221> polyA_signal
<222> 2786..2791

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<220>
<221> polyA_site
<222> 2804..2818

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<400> 39
ggcttttgggg cagggcagat ttatatctgc gggggatcag ctgacgctcc gcattgcaga 60
ctgcggagtc agacggcgct atg tac gcc ctc ttc ctc ctg gcc agc ctc ctg 113
                Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu
                1                5                10
ggc gcg gct cta gcc ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg 161
Gly Ala Ala Leu Ala Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg
                15                20                25
ggc tcg gca gtg tgg tgc cag aat gtg aag acg gcg tcc gac tgc ggg 209
Gly Ser Ala Val Trp Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly
                30                35                40
gca gtg aag cac tgc ctg cag acc gtt tgg aac aag cca aca gtg aaa 257
Ala Val Lys His Cys Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys
                45                50                55
tcc ctt ccc tgc gac ata tgc aaa gac gtt gtc acc gca gct ggt gat 305
Ser Leu Pro Cys Asp Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp

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60	atg ctg aag gac aat gcc act gag gag gag atc ctt gtt tac ttg gag	65	80	70	85	75	90	353
	Met Leu Lys Asp Asn Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu							
	aag acc tgt gac tgg ctt ccg aaa ccg aac atg tct gct tca tgc aag		80		85		90	401
	Lys Thr Cys Asp Trp Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys							
	gag ata gtg gac tcc tac ctc cct gtc atc ctg gac atc att aaa gga		95		100		105	449
	Glu Ile Val Asp Ser Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly							
	gaa atg agc cgt cct ggg gag gtg tgc tct gct ctc aac ctc tgc gag		110		115		120	497
	Glu Met Ser Arg Pro Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu							
	tct ctc cag aag cac cta gca gag ctg aat cac cag aag cag ctg gag		125		130		135	545
	Ser Leu Gln Lys His Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu							
	tcc aat aag atc cca gag ctg gac atg act gag gtg gtg gcc ccc ttc		140		145		150	593
	Ser Asn Lys Ile Pro Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe							
	atg gcc aac atc cct ctc ctc ctc tac cct cag gac ggc ccc cgc agc		160		165		170	641
	Met Ala Asn Ile Pro Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser							
	aag ccc cag cca aag gat aat ggg gac gtt tgc cag gac tgc att cag		175		180		185	689
	Lys Pro Gln Pro Lys Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln							
	atg gtg act gac atc cag act gct gta cgg acc aac tcc acc ttt gtc		190		195		200	737
	Met Val Thr Asp Ile Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val							
	cag gcc ttg gtg gaa cat gtc aag gag gag tgt gac cgc ctg ggc cct		205		210		215	785
	Gln Ala Leu Val Glu His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro							
	ggc atg gcc gac ata tgc aag aac tat atc agc cag tat tct gaa att		220		225		230	833
	Gly Met Ala Asp Ile Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile							
	gct atc cag atg atg atg cac atg cag gat cag caa ccc aag gag atc		240		245		250	881
	Ala Ile Gln Met Met Met His Met Gln Asp Gln Gln Pro Lys Glu Ile							
	tgt gcg ctg gtt ggg ttc tgt gat gag gtg aaa gag atg ccc atg cag		255		260		265	929
	Cys Ala Leu Val Gly Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln							
	act ctg gtc ccc gcc aaa gtg gcc tcc aag aat gtc atc cct gcc ctg		270		275		280	977
	Thr Leu Val Pro Ala Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu							
	gaa ctg gtg gag ccc att aag aag cac gag gtc cca gca aag tct gat		285		290		295	1025
	Glu Leu Val Glu Pro Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp							
	gtt tac tgt gag gtg tgt gaa ttc ctg gtg aag gag gtg acc aag ctg		300		305		310	1073
	Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu							
	att gac aac aac aag act gag aaa gaa ata ctc gac gct ttt gac aaa		320		325		330	1121
	Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys							
	atg tgc tcg aag ctg ccg aag tcc ctg tcg gaa gag tgc cag gag gtg		335		340		345	1169
	Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val							
	gtg gac acg tac ggc agc tcc atc ctg tcc atc ctg ctg gag gag gtc		350		355		360	1217

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Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val
  365                      370                      375
agc cct gag ctg gtg tgc agc atg ctg cac ctc tgc tct ggc acg cgg 1265
Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg
  380                      385                      390                      395
ctg cct gca ctg acc gtt cac gtg act cag cca aag gac ggt ggc ttc 1313
Leu Pro Ala Leu Thr Val His Val Thr Gln Pro Lys Asp Gly Gly Phe
                      400                      405                      410
tgc gaa gtg tgc aag aag ctg gtg ggt tat ttg gat cgc aac ctg gag 1361
Cys Glu Val Cys Lys Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu
                      415                      420                      425
aaa aac agc acc aag cag gag atc ctg gct gct ctt gag aaa ggc tgc 1409
Lys Asn Ser Thr Lys Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys
                      430                      435                      440
agc ttc ctg cca gac cct tac cag aag cag tgt gat cag ttt gtg gca 1457
Ser Phe Leu Pro Asp Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala
                      445                      450                      455
gag tac gag ccc gtg ctg atc gag atc ctg gtg gag gta tgg atc ctt 1505
Glu Tyr Glu Pro Val Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu
  460                      465                      470                      475
cct tcg tgt gct tgaaaattgg agcctgcccc tcggcccata agcccttggt 1557
Pro Ser Cys Ala
gggaactgag aagtgtatat ggggcccagg ctactgggtgc cagaacacag agacagcagc 1617
ccagtgcaat gctgtcgagc attgcaaacg ccatgtgtgg aactaggagg aggaatattc 1677
catcttggca gaaaccacag cattggtttt tttctacttg tgtgtctggg ggaatgaacg 1737
cacagatctg tttagactttg ttataaaaaat agggctcccc cacctcccc atttctgtgt 1797
cctttattgt agcattgctg tctgcaaggg agcccctagc ccctggcaga catagctgtc 1857
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ccttgcatgg cgcctgctgg aggaggagag agctctgctg gcatgagcca cagtctcttg 1977
actggaggcc atcaaccctc ttggttgagg ccttggtctg agccctgaca tgtgcttggg 2037
cactgggtgg cctgggcttc tgaggtggcc tcctgccctg atcaggggacc ctccccgctt 2097
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<210> 40

<211> 479

<212> PRT

<213> Homo sapiens

<400> 40

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Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
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Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
                      20                      25                      30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys

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35	40	45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp		
50	55	60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn		
65	70	75
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp		
85	90	95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser		
100	105	110
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro		
115	120	125
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His		
130	135	140
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro		
145	150	155
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro		
165	170	175
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys		
180	185	190
Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile		
195	200	205
Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu		
210	215	220
His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile		
225	230	235
Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met		
245	250	255
Met His Met Gln Asp Gln Gln Pro Lys Glu Ile Cys Ala Leu Val Gly		
260	265	270
Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala		
275	280	285
Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro		
290	295	300
Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val		
305	310	315
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys		
325	330	335
Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu		
340	345	350
Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly		
355	360	365
Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val		
370	375	380
Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr		
385	390	395
Val His Val Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys		
405	410	415
Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys		
420	425	430
Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp		
435	440	445
Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val		
450	455	460
Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu Pro Ser Cys Ala		
465	470	475

<210> 41
 <211> 770
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..120

<220>
 <221> CDS
 <222> 121..546

<220>
 <221> 3'UTR
 <222> 547..770

<220>
 <221> polyA_signal
 <222> 739..744

<220>
 <221> polyA_site
 <222> 755..770

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<400> 41
cttttcttgg gctctaagga cccaggagtc tgggtgcaca gcctccttct ctctgagatt 60
caagagtctg atcagcagcc tcttctctct ccaggaccca gaagccctga gcttatcccc 120
atg gag ctg tgc cgg tcc ctg gcc ctg ctg ggg ggc tcc ctg ggc ctg 168
Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu
      -35              -30              -25
atg ttc tgc ctg att gct ttg agc acc gat ttc tgg ttt gag gct gtg 216
Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
      -20              -15              -10
ggg ccc acc cac tca gct cac tcg ggc ctc tgg cca aca ggg cat ggg 264
Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
      -5              1              5              10
gac atc ata tca ggc cac ggc ccg ctt gtc tca acc acc gca gcc ttt 312
Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe
      15              20              25
gct gca ggt aag gac tct gga ctg gac tgg ggc atc gcg agc cag cga 360
Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
      30              35              40
att cct gcc gag gag ctg agc cat ctc tct tgt cct tgt ccc cag cca 408
Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
      45              50              55
tct cca tgg tgg tgg cca tgg cgg tgt aca cca gcg agc ggt ggg acc 456
Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
      60              65              70              75
agc ctc cac acc ccc aga tcc aga cct tct tct cct ggt cct tct acc 504
Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
      80              85              90
tgg gct ggg tct cag cta tcc tct tgc tct gta cag gtg ccc 546
Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
      95              100              105
tgagcctggg tgctcactgt ggcgggtcccc gtccctggcta tgaaaccttg tgagcagaag 606

```

```

gcaagagcgg caagatgagt tttgagcggt gtattccaaa ggctcatct ggagcctcgg 666
gaaagtctgg tcccacatct gccgcctt ccagccttc cccagccct cctcttggtt 726
cttcattcat tcaacaaaat ttggctggaa aaaaaaaaaa aaaa 770

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<210> 42
<211> 142
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..37

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<400> 42
Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu
      -35                      -30                      -25
Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
      -20                      -15                      -10
Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
      -5                      1                      5                      10
Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe
      15                      20                      25
Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
      30                      35                      40
Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
      45                      50                      55
Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
      60                      65                      70                      75
Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
      80                      85                      90
Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
      95                      100                      105

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<210> 43
<211> 1340
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..135

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<220>
<221> CDS
<222> 136..501

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<220>
<221> 3'UTR
<222> 502..1340

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<220>
<221> polyA_signal
<222> 1232..1237

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<220>
<221> polyA_site

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<222> 1255..1340

<400> 43

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ctcttttggg gttcttccctt tctctctcag ctctccgtct ctctttctct ctcagcctct 60
ttctttctcc ctgtctcccc cactgtcagc acctcttctg tgtggtgagt ggaccgctta 120
ccccactagg tgaag atg tca gcc cag gag agc tgc ctc agc ctc atc aag 171
          Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys
                1             5             10
tac ttc ctc ttc gtt ttc aac ctc ttc ttc ttc gtc ctc ggc agc ctg 219
Tyr Phe Leu Phe Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu
          15             20             25
atc ttc tgc ttc ggc atc tgg atc ctc att gac aag acc agc ttc gtg 267
Ile Phe Cys Phe Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val
          30             35             40
tcc ttt gtg ggc ttg gcc ttc gtg cct ctg cag atc tgg tcc aaa gtc 315
Ser Phe Val Gly Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val
          45             50             55             60
ctg gcc atc tca gga atc ttc acc atg ggc atc gcc ctc ctg ggt tgt 363
Leu Ala Ile Ser Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys
          65             70             75
gtg ggg gcc ctc aag gag ctc cgc tgc ctc ctg ggc ctg tat ttt ggg 411
Val Gly Ala Leu Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly
          80             85             90
atg ctg ctg ctc ctg ttt gcc aca cag atc acc ctg gga atc ctc atc 459
Met Leu Leu Leu Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile
          95             100             105
tcc act cag cgg gcc agc tgg agc gaa gct tgc ggg acg tcg 501
Ser Thr Gln Arg Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser
          110             115             120
tagagaaaac catccaaaag tacggcacca accccgagga gaccgcggcc gaggagagct 561
gggactatgt gcagttccag ctgcgctgct gcggctggca ctaccgcag gactggttcc 621
aagtcctcat cctgagaggt aacgggtcgg aggcgcaccg cgtgccctgc tcctgctaca 681
acttgctggc gaccaacgac tccacaatcc tagataaggt gatcttgccc cagctcagca 741
ggcttggaac cctggcgagg tccagacaca gtgcagacat ctgcgctgtc cctgcagaga 801
gccacatcta ccgcgagggc tgcgcgcagg gcctccagaa gtggctgcac aacaacctta 861
tttccatagt gggcatttgc ctgggcgtcg gcctactcga gctcgggttc atgacgctct 921
cgatattcct gtgcagaaac ctggaccacg tctacaaccg gctcgcctcga taccgttagg 981
ccccgcctc cccaaagtcc cgccccgccc ccgtcacgtg cgctgggcac ttccctgctg 1041
cctgtaaaata tttgtttaat ccccagttcg cctggagccc tctccttca cattcccctg 1101
gggacccacg tggctgcgtg cccctgctgc tgtaacctct cccacgggac ctggggcttt 1161
cgtccacagc ttctgtgcc catctgtcgg cctaccacca cccacaagat tatttttcac 1221
ccaaacctca aataaatccc ctgcgttttt ggtaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1281
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa amcaaaaaaaaa aaaaaaaaaa 1340

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<210> 44

<211> 122

<212> PRT

<213> Homo sapiens

<400> 44

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Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1             5             10             15
Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
          20             25             30
Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
          35             40             45

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Leu	Ala	Phe	Val	Pro	Leu	Gln	Ile	Trp	Ser	Lys	Val	Leu	Ala	Ile	Ser
50						55					60				
Gly	Ile	Phe	Thr	Met	Gly	Ile	Ala	Leu	Leu	Gly	Cys	Val	Gly	Ala	Leu
65					70					75					80
Lys	Glu	Leu	Arg	Cys	Leu	Leu	Gly	Leu	Tyr	Phe	Gly	Met	Leu	Leu	Leu
				85					90					95	
Leu	Phe	Ala	Thr	Gln	Ile	Thr	Leu	Gly	Ile	Leu	Ile	Ser	Thr	Gln	Arg
			100					105					110		
Ala	Ser	Trp	Ser	Glu	Ala	Cys	Gly	Thr	Ser						
		115					120								

<210> 45

<211> 1999

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..117

<220>

<221> CDS

<222> 118..1632

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<221> 3'UTR

<222> 1633..1999

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<221> polyA_signal

<222> 1937..1942

<220>

<221> polyA_site

<222> 1956..1999

<400> 45

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tcc	gc	ag	tcc	cag	ccg	ag	acc	ctt	cgg	ccg	tccc	cac	cccc	acct	cg	ccg	cc				117
atg	cg	ctc	cg	cg	cta	gcg	ctg	ttc	ccg	ggt	gtg	gcg	ctg	ctt	ctt						165
Met	Arg	Leu	Arg	Arg	Leu	Ala	Leu	Phe	Pro	Gly	Val	Ala	Leu	Leu	Leu						
				-20					-15					-10							
gcc	gcg	gcc	cg	ctc	gcc	gct	gcc	tcc	gac	gtg	cta	gaa	ctc	acg	gac						213
Ala	Ala	Ala	Arg	Leu	Ala	Ala	Ala	Ser	Asp	Val	Leu	Glu	Leu	Thr	Asp						
			-5					1			5										
gac	aac	ttc	gag	agt	cg	atc	tcc	gac	acg	ggc	tct	gcg	ggc	ctc	atg						261
Asp	Asn	Phe	Glu	Ser	Arg	Ile	Ser	Asp	Thr	Gly	Ser	Ala	Gly	Leu	Met						
	10					15				20											
ctc	gtc	gag	ttc	ttc	gct	ccc	tgg	tgt	gga	cac	tgc	aag	aga	ctt	gca						309
Leu	Val	Glu	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Arg	Leu	Ala						
	25				30				35					40							
cct	gag	tat	gaa	gct	gca	gct	acc	aga	tta	aaa	gga	ata	gtc	cca	tta						357
Pro	Glu	Tyr	Glu	Ala	Ala	Ala	Thr	Arg	Leu	Lys	Gly	Ile	Val	Pro	Leu						
				45				50					55								
gca	aag	gtt	gat	tgc	act	gcc	aac	act	aac	acc	tgt	aat	aaa	tat	gga						405
Ala	Lys	Val	Asp	Cys	Thr	Ala	Asn	Thr	Asn	Thr	Cys	Asn	Lys	Tyr	Gly						

gtc	agt	gga	tat	cca	acc	ctg	aag	ata	ttt	aga	gat	ggt	gaa	gaa	gca	453
Val	Ser	Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Asp	Gly	Glu	Glu	Ala	
		75					80					85				
ggt	gct	tat	gat	gga	cct	agg	act	gct	gat	gga	att	gtc	agc	cac	ttg	501
Gly	Ala	Tyr	Asp	Gly	Pro	Arg	Thr	Ala	Asp	Gly	Ile	Val	Ser	His	Leu	
		90					95				100					
aag	aag	cag	gca	gga	cca	gct	tca	gtg	cct	ctc	agg	act	gag	gaa	gaa	549
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu	
105					110					115					120	
ttt	aag	aaa	ttc	att	agt	gat	aaa	gat	gcc	tct	ata	gta	ggt	ttt	ttc	597
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe	
				125					130					135		
gat	gat	tca	ttc	agt	gag	gct	cac	tcc	gag	ttc	cta	aaa	gca	gcc	agc	645
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser	
			140				145						150			
aac	ttg	agg	gat	aac	tac	cga	ttt	gca	cat	acg	aat	gtt	gag	tct	ctg	693
Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu	
		155					160						165			
gtg	aac	gag	tat	gat	gat	aat	gga	gag	ggt	atc	atc	tta	ttt	cgt	cct	741
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro	
		170				175						180				
tca	cat	ctc	act	aac	aag	ttt	gag	gac	aag	act	gtg	gca	tat	aca	gag	789
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu	
185					190					195					200	
caa	aaa	atg	acc	agt	ggc	aaa	att	aaa	aag	ttt	atc	cag	gaa	aac	att	837
Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile	
				205					210					215		
ttt	ggt	atc	tgc	cct	cac	atg	aca	gaa	gac	aat	aaa	gat	ttg	ata	cag	885
Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln	
			220						225				230			
ggc	aag	gac	tta	ctt	att	gct	tac	tat	gat	gtg	gac	tat	gaa	aag	aac	933
Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn	
		235				240						245				
gct	aaa	ggt	tcc	aac	tac	agg	aga	aac	agg	gta	atg	atg	gtg	gca	aag	981
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys	
		250				255						260				
aaa	ttc	ctg	gat	gct	ggg	cac	aaa	ctc	aac	ttt	gct	gta	gct	agc	cgc	1029
Lys	Phe	Leu	Asp	Ala	Gly	His	Lys	Leu	Asn	Phe	Ala	Val	Ala	Ser	Arg	
265					270					275					280	
aaa	acc	ttt	agc	cat	gaa	ctt	tct	gat	ttt	ggc	ttg	gag	agc	act	gct	1077
Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala	
				285					290					295		
gga	gag	att	cct	ggt	ggt	gct	atc	aga	act	gct	aaa	gga	gag	aag	ttt	1125
Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe	
			300					305					310			
gtc	atg	cag	gag	gag	ttc	tcg	cgt	gat	ggg	aag	gct	ctg	gag	agg	ttc	1173
Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe	
		315						320					325			
ctg	cag	gat	tac	ttt	gat	ggc	aat	ctg	aag	aga	tac	ctg	aag	tct	gaa	1221
Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu	
		330				335					340					
cct	atc	cca	gag	agc	aat	gat	ggg	cct	gtg	aag	gta	gtg	gta	gca	gag	1269
Pro	Ile	Pro	Glu	Ser	Asn	Asp	Gly	Pro	Val	Lys	Val	Val	Val	Ala	Glu	
345					350					355					360	
aat	ttt	gat	gaa	ata	gtg	aat	aat	gaa	aat	aaa	gat	gtg	ctg	att	gaa	1317


```

Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
      365      370      375
ttt tat gcc cct tgg tgt ggt cat tgt aag aac ctg gag ccc aag tat 1365
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
      380      385      390
aaa gaa ctt ggc gag aag ctc agc aaa gac cca aat atc gtc ata gcc 1413
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
      395      400      405
aag atg gat gcc aca gcc aat gat gtg cct tct cca tat gaa gtc aga 1461
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
      410      415      420
ggg ttt cct acc ata tac ttc tct cca gcc aac aag aag cta aat cca 1509
Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
      425      430      435      440
aag aaa tat gaa ggt ggc cgt gaa tta agt gat ttt att agc tat cta 1557
Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
      445      450      455
caa aga gaa gct aca atc ccc cct gta att caa gaa gaa aaa ccc aag 1605
Gln Arg Glu Ala Thr Ile Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
      460      465      470
aag aag aag aag gca cag gag gat ctc taaagcagta gccaaacacc 1652
Lys Lys Lys Lys Ala Gln Glu Asp Leu
      475      480
actttgtaaa aggactcttc catcagagat gggaaaaacca ttggggagga ctaggaccca 1712
tatgggaatt attacctctc agggccgaga ggacagaatg gatataatct gaatcctgtt 1772
aaattttctc taaactgttt cttagctgca ctgtttatgg aaataccagg accagtttat 1832
gtttgtggtt ttgggaaaaa ttatttgtgt tgggggaaat gttgtggggg tggggttgag 1892
ttgggggtat tttctaattt tttttgtaca tttggaacag tgacaataaa tgagaccctt 1952
tttaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaawaaaa aaaaaaa 1999

```

<210> 46

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..24

<400> 46

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Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu
      -20      -15      -10
Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
      -5      1      5
Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
      10      15      20
Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
      25      30      35      40
Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
      45      50      55
Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
      60      65      70
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
      75      80      85
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu
      90      95      100

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Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu
105          110          115          120
Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe
          125          130          135
Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser
          140          145          150
Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu
          155          160          165
Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro
          170          175          180
Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu
185          190          195          200
Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile
          205          210          215
Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln
          220          225          230
Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn
          235          240          245
Ala Lys Gly Ser Asn Tyr Arg Arg Asn Arg Val Met Met Val Ala Lys
          250          255          260
Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg
265          270          275          280
Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala
          285          290          295
Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe
          300          305          310
Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe
          315          320          325
Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu
          330          335          340
Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu
345          350          355          360
Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
          365          370          375
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
          380          385          390
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
          395          400          405
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
          410          415          420
Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
425          430          435          440
Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
          445          450          455
Gln Arg Glu Ala Thr Ile Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
          460          465          470
Lys Lys Lys Lys Ala Gln Glu Asp Leu
          475          480

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<210> 47

<211> 836

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..153

<220>

<221> CDS

<222> 154..546

<220>

<221> 3'UTR

<222> 547..836

<220>

<221> polyA_site

<222> 722..836

<400> 47

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accctccct ggccccgcc tcccggactc ctgaccaaat gacccccccc ggcaggtgtt 60
tcgcccgtgc cgggttcattg ctcacaagca gacagctcct ccgcctctga tgcagaattt 120
gatgctgtgg ttggatattt agaggacatt atc atg gat gac gag ttc cag tta 174
                               Met Asp Asp Glu Phe Gln Leu
                               1           5

tta cag aga aat ttc atg gac aag tac tac ctg gag ttt gaa gac aca 222
Leu Gln Arg Asn Phe Met Asp Lys Tyr Tyr Leu Glu Phe Glu Asp Thr
      10           15           20

gaa gag aat aaa ctc atc tac aca cct att ttt aat gaa tac att tct 270
Glu Glu Asn Lys Leu Ile Tyr Thr Pro Ile Phe Asn Glu Tyr Ile Ser
      25           30           35

ttg gta gaa aaa tac att gaa gaa cag ctg ctg cag cgg att cct gag 318
Leu Val Glu Lys Tyr Ile Glu Glu Gln Leu Leu Gln Arg Ile Pro Glu
      40           45           50           55

ttc aac atg gca gcc ttc acc aca aca tta cag cac cat aag gat gaa 366
Phe Asn Met Ala Ala Phe Thr Thr Thr Leu Gln His His Lys Asp Glu
      60           65           70

gtg gct ggt gac ata ttc gac atg ctg ctc acc ttc aca gat ttt ctg 414
Val Ala Gly Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu
      75           80           85

gct ttt aaa gaa atg ttt ttg gac tac aga gca gaa aaa gaa ggc cga 462
Ala Phe Lys Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg
      90           95          100

gga ctg gac tta agc agt ggc tta gtg gtg act tca ttg tgc aaa tca 510
Gly Leu Asp Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser
     105          110          115

tct tct ctg cca gct tcc cag aac aat ctg cgg cac taggtcctac 556
Ser Ser Leu Pro Ala Ser Gln Asn Asn Leu Arg His
     120          125          130

ctccagccaa tgaatgggat cattctggat gtcaccagcc caataggctc agctcatgat 616
gacagaacac atcttggaaa gactgactct gttatgtaac tcttcattta tgttaagtat 676
taatagggtca aaaccaaata gacctaacct tcttggacct atttcaaaaa aaaaaaaaaa 736
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 796
aaaaaaaaaa aaaaaaaaaa aaaagaaaaa aaaaaaaaaa 836

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<210> 48

<211> 131

<212> PRT

<213> Homo sapiens

<400> 48

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Met Asp Asp Glu Phe Gln Leu Leu Gln Arg Asn Phe Met Asp Lys Tyr
1          5          10          15
Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro
          20          25          30
Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln
          35          40          45
Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr
          50          55          60
Leu Gln His His Lys Asp Glu Val Ala Gly Asp Ile Phe Asp Met Leu
65          70          75          80
Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys Glu Met Phe Leu Asp Tyr
          85          90          95
Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp Leu Ser Ser Gly Leu Val
          100          105          110
Val Thr Ser Leu Cys Lys Ser Ser Ser Leu Pro Ala Ser Gln Asn Asn
          115          120          125
Leu Arg His
          130

```

```

<210> 49
<211> 862
<212> DNA
<213> Homo sapiens

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```

<220>
<221> 5'UTR
<222> 1..195

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<220>
<221> CDS
<222> 196..708

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<220>
<221> 3'UTR
<222> 709..862

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<220>
<221> polyA_site
<222> 847..862

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<400> 49
ttcgcacctc ggagctggaa atgcagctat tgagatcttc gaatgctgcg gagctggagg 60
cggaggcgagc tggggagggtc cgagcgatgt gaccaggccg ccatcgctcg tctcttcctc 120
tctcctgccc cctcctgtct cgtaaataac ttttttactc taaagaaaga aagacaaaag 180
tagtcgtccg ccccc atg cat ccc ttc tac acc cgg gcc gcc acc atg ata 231
          Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile
          1          5          10
ggc gag atc gcc gcc gcc gtg tcc ttc atc tcc aag ttt ctc cgc acc 279
Gly Glu Ile Ala Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr
          15          20          25
aag ggg ctc acg agc gag cga cag ctg cag acc ttc agc cag agc ctg 327
Lys Gly Leu Thr Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu
          30          35          40
cag gag ctg ctg gca gaa cat tat aaa cat cac tgg ttc cca gaa aag 375
Gln Glu Leu Leu Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys
          45          50          55          60

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cca tgc aag gga tgc ggt tac cgt tgt att cgc atc aac cat aaa atg 423
Pro Cys Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met
                        65                        70                        75
gat cct ctg att gga cag gca gca cag cgg att gga ctg agc agt cag 471
Asp Pro Leu Ile Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln
                        80                        85                        90
gag ctg ttc agg ctt ctc cca agt gaa ctc aca ctc tgg gtt gac ccc 519
Glu Leu Phe Arg Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro
                        95                        100                        105
tat gaa gtg tcc tac aga att gga gag gat ggc tcc atc tgt gtg ctg 567
Tyr Glu Val Ser Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu
                        110                        115                        120
tat gaa gcc tca cca gca gga ggt agc act caa aac agc acc aac gtg 615
Tyr Glu Ala Ser Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val
125                        130                        135                        140
caa atg gta gac agc cga atc agc tgt aag gag gaa ctt ctc ttg ggc 663
Gln Met Val Asp Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu Gly
                        145                        150                        155
aga acg agc cct tcc aaa aac tac aat atg atg act gta tca agt 708
Arg Thr Ser Pro Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser
                        160                        165                        170
taagatatag tctgtggatg gatcatctga tgatgatgga taaatttgat ttttgctttg 768
ggtgggctcc tcttggggat ggattatgga atttaaacca tgtcacagct gtgaagatct 828
ggcacaagat agaatggcaa aaaaaaaaaa aaaa 862

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<210> 50

<211> 171

<212> PRT

<213> Homo sapiens

<400> 50

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Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile Gly Glu Ile Ala
1                        5                        10                        15
Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr Lys Gly Leu Thr
20                        25                        30
Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu Gln Glu Leu Leu
35                        40                        45
Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys Pro Cys Lys Gly
50                        55                        60
Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Leu Ile
65                        70                        75                        80
Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln Glu Leu Phe Arg
85                        90                        95
Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser
100                        105                        110
Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Ala Ser
115                        120                        125
Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val Gln Met Val Asp
130                        135                        140
Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu Gly Arg Thr Ser Pro
145                        150                        155                        160
Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser
165                        170

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<210> 51

<211> 947

<212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..61

<220>
 <221> CDS
 <222> 62..778

<220>
 <221> 3'UTR
 <222> 779..947

<220>
 <221> polyA_signal
 <222> 912..917

<220>
 <221> polyA_site
 <222> 932..947

<400> 51
 gaggaaagag tcacagagg gatcagcagc tccaggggaag gcctggctgc cccgcttcta 60
 a atg cca ctc ccc ctc cca tca gcg ttc gtg ctg tca gcc ttg cag cct 109
 Met Pro Leu Pro Leu Pro Ser Ala Phe Val Leu Ser Ala Leu Gln Pro
 -20 -15 -10
 tct cct act cat tcc agc tcc aat acc cag cgg ctg cca gac cga gtg 157
 Ser Pro Thr His Ser Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val
 -5 1 5 10
 acc ggc ggc ttc tca gtg aat gga cag ctc att ggc aac aag gcc agg 205
 Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg
 15 20 25
 agc cct ggg cag cat gac ggc acg tac ttc ggg cgg ctg gga atc gca 253
 Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
 30 35 40
 aac cct gcc acg gac ttt cag ttg gaa gtg act cct cag aac att acg 301
 Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr
 45 50 55
 ctg aac ccc ggc ttt ggt ggg cct gtg ttt tcc tgg agg gac caa gct 349
 Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala
 60 65 70 75
 gtg ctg cgg cag gac ggg gtg gtg gtg acc atc aac aag aag agg aac 397
 Val Leu Arg Gln Asp Gly Val Val Val Thr Ile Asn Lys Lys Arg Asn
 80 85 90
 ctg gtg gtg tct gtg gac gac ggt ggc acc ttt gag gtt gtt ttg cac 445
 Leu Val Val Ser Val Asp Asp Gly Gly Thr Phe Glu Val Val Leu His
 95 100 105
 cga gtg tgg aag ggg agc tcg gtc cac cag gac ttc ctg ggc ttc tat 493
 Arg Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr
 110 115 120
 gtg ctg gac agt cat cgg atg tca gcc cgg acg cac ggg ctg ctg ggg 541
 Val Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly
 125 130 135
 caa ttt ttc cac ccc atc ggt ttt gaa gtg tct gac atc cac cca ggc 589

```

Gln Phe Phe His Pro Ile Gly Phe Glu Val Ser Asp Ile His Pro Gly
140          145          150          155
tct gac ccc aca aag cca gat gcc acg atg gtg gtg agg aac cgc cgg 637
Ser Asp Pro Thr Lys Pro Asp Ala Thr Met Val Val Arg Asn Arg Arg
          160          165          170
ctc acg gtc acc agg ggt ttg caa aaa gac tac agc aag gac ccg tgg 685
Leu Thr Val Thr Arg Gly Leu Gln Lys Asp Tyr Ser Lys Asp Pro Trp
          175          180          185
cat ggg gcc gag gtg tcc tgc tgg ttc att cac aac aat ggg gct gga 733
His Gly Ala Glu Val Ser Cys Trp Phe Ile His Asn Asn Gly Ala Gly
          190          195          200
ctc atc gat ggt gcc tac act gat tat atc gtc ccc gac atc ttc 778
Leu Ile Asp Gly Ala Tyr Thr Asp Tyr Ile Val Pro Asp Ile Phe
          205          210          215
tgagccctct ggccagcacg cctgtcctcc cccggggcca aggcagagga ggaggacgac 838
atcctgacct gctgctgagg ctgtacctcc ttgactaagc tggttccttg tgtcaaagca 898
cctcatgcct tccattaaag agaggccgtg tccaaaaaaaa aaaaaaaaaa 947

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<210> 52

<211> 239

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..21

<400> 52

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Met Pro Leu Pro Leu Pro Ser Ala Phe Val Leu Ser Ala Leu Gln Pro
-20          -15          -10
Ser Pro Thr His Ser Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val
-5          1          5          10
Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg
          15          20          25
Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
          30          35          40
Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr
          45          50          55
Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala
60          65          70          75
Val Leu Arg Gln Asp Gly Val Val Val Thr Ile Asn Lys Lys Arg Asn
          80          85          90
Leu Val Val Ser Val Asp Asp Gly Gly Thr Phe Glu Val Val Leu His
          95          100          105
Arg Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr
          110          115          120
Val Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly
          125          130          135
Gln Phe Phe His Pro Ile Gly Phe Glu Val Ser Asp Ile His Pro Gly
140          145          150          155
Ser Asp Pro Thr Lys Pro Asp Ala Thr Met Val Val Arg Asn Arg Arg
          160          165          170
Leu Thr Val Thr Arg Gly Leu Gln Lys Asp Tyr Ser Lys Asp Pro Trp
          175          180          185
His Gly Ala Glu Val Ser Cys Trp Phe Ile His Asn Asn Gly Ala Gly
          190          195          200

```

Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile	Phe
205						210					215			